

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:22 ; Search time 31 Seconds  
 Sequence: (without alignments)  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Title: US-10-743-697-1  
 Perfect score: 1  
 Sequence: ELVMTQSPSSLTIVTAGEKVT.....LDYWGQGTTLVSSHHHHHH 378  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched:

572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database : Issued Patents AA,\*

1: /cgn2\_6/ptodata/1/iaa/5/COMB.pep: \*  
 2: /cgn2\_6/ptodata/1/iaa/6/COMB.pep: \*  
 3: /cgn2\_6/ptodata/1/iaa/H/COMB.pep: \*  
 4: /cgn2\_6/ptodata/1/iaa/PCUTUS/COMB.pep: \*  
 5: /cgn2\_6/ptodata/1/iaa/RE/COMB.pep: \*  
 6: /cgn2\_6/ptodata/1/iaa/bactfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1484.5	72.6	495	2	US-09-948-004-18
2	1287.5	62.9	553	1	US-08-363-911-9
3	1283	62.7	483	1	US-08-392-180A-19
4	1283	62.7	483	2	US-09-166-710-19
5	1283	62.7	483	2	US-09-166-013-19
6	1283	62.7	483	2	US-09-172-019-19
7	1283	62.7	483	2	US-09-166-004-19
8	1283	62.7	483	2	US-09-433-213-19
9	1230.5	60.1	553	1	US-09-263-911-7
10	955	46.7	456	2	US-09-495-800A-11
11	938	45.8	249	2	US-09-059-821-2
12	938	45.8	249	2	US-09-956-086-2
13	938	45.8	249	2	US-09-056-007-2
14	938	45.8	354	2	US-09-323-621B-28
15	937	45.8	257	2	US-09-220-592A-2
16	937	45.8	257	2	US-09-985-412-2
17	937	45.8	257	2	US-09-993-580-2
18	937	45.8	257	2	US-09-554-04-4
19	937	45.8	257	2	US-09-791-578-4
20	937	45.8	269	2	US-09-420-592A-4
21	937	45.8	269	2	US-09-985-442-4
22	937	45.8	269	2	US-09-983-580-4
23	929	45.4	241	2	US-09-791-578-6
24	929	45.4	262	1	US-08-323-442A-4
25	929	45.4	262	1	US-08-515-903A-4
26	929	45.4	262	1	PCT-US95-12840-4
27	929	45.4	262	4	PCT-US95-12840-4

### ALIGNMENTS

RESULT 1  
 US-09-948-004-18  
 Sequence 18, Application US/09948004  
 Patent No. 672358  
 GENERAL INFORMATION:  
 APPLICANT: MACK, Matthias  
 TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in  
 TITLE OF INVENTION: Immunological disorders  
 FILE REFERENCE: E 2411 EP  
 CURRENT APPLICATION NUMBER: US/09/948, 004  
 CURRENT FILING DATE: 2001-09-05  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 18  
 LENGTH: 495  
 TYPE: PRT  
 ORGANISM: Mus sp.  
 US-09-948-004-18

Query Match 72.6%; Score 1484.5; DB 2; Length 495;

Best Local Similarity 74.7%; Pred. No. 2.4e-102; Mismatches 53; Indels 7; Gaps 2;

Matches 278; Conservative 34; Score 1484.5; DB 2; Length 495;

Query

1 BLVMTQSPSSLTIVTAGEKVTMSCKSQSSLNSNGNQKNLYTWQKQGQPPLKLIWASTR

60

1 DIVLVTQSPASLSSAQSVTGTTICRASENN-----SYLAWYQQKOKSPQQLIVNAKTL

54

2 ESGVPRFTGGSGGTFETLTTSSVQEDLATYCONDYSVLTGGAGKTBIGGSGGG

120

3 TEGVPRFRSGSGSGTORSFLSKINSLQPBDFGNVFCOHRYDTPRTFGGGTKEIKGGGG

114

4 121 GSGGGGGSEVQLEQSGAELVRPGTYSKISKASGKFTNWLGMKQRCGHLGMDI

180

5 115 GSGGGGGSQVQLQPGAGTRPGASVTKLSCASGYSFTSYNNWYKRPQPGOLEWGM

173

6 181 FPGSGNHYNEKPKGKATLTDKSSSTAYMQLSSLTFSDEAVYFCARLNNIDBPMWQ

240

7 174 HPSDSETRLNQKENDRATITUDKYSSTAYIQLSSPSEDASVYCARDDYFDWQ

233

8 Db

9 241 GRTVTVSSGGGGSDIKQOSGAEELPGASVYCNKSGYFTYRTHWVKORGQCLEW

300

10 234 GRTVTVSSGGGGSDIKQOSGAEELPGASVYCNKSGYFTYRTHWVKORGQCLEW

293

11 QY

12 301 IGYINPRSGYTYNQKFKKATLTTKSSSTAYMQLSSLTFSDEAVYCARDDYFDWQ

360

13 Db

14 294 IGYINPRSGYTYNQKFKKATLTTDSSSTAYMQLSSLTFSDEAVYCARDDYFDWQ

353

15 QY

16 361 YNGQGTTLVSS

372

17 Db

18 354 YNRQGTTLVSS

365

RESULT 2  
 US-08-263-911-9  
 Sequence 9, Application US/08263911  
 ; Patient No. 5877291  
 GENERAL INFORMATION:  
 ; APPLICANT: Mezes, Peter S  
 ; TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Duane C. Ulmer  
 ; STREET: P.O. Box 1967  
 ; CITY: Midland  
 ; STATE: MI  
 ; COUNTRY: US  
 ; ZIP: 48641-1967  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/263, 911  
 FILING DATE: 21-JUN-1994  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/990, 263  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ulmer, Duane C  
 REFERENCE/DOCKET NUMBER: 34, 941  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 636-8104  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 553 amino acids  
 TYPE: amino acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 23

Query Match  
 Best local Similarity 64.2%; Score 1287.5; DB 1; length 553;  
 Matches 258; Conservative 37; Mismatches 68; Indels 39; Gaps 5;

QY 1 ELYWQPSLTLVTAEGKVTMSCKSSQSLLNSNQKNTLTWQPKGQPKPLIYWASTR 60  
 23 DIVMSQSPSILPVSVGKVKLTSCKSSQSLLNSNQKNTLYAWQPKGQSPKPLIYWASR 82

Db 23 DIVMSQSPSILPVSVGKVKLTSCKSSQSLLNSNQKNTLYAWQPKGQSPKPLIYWASR 82

QY 61 ESGVDPDRFGSGSGTDFLTISVQAEELAVYQNDSYPLTGAIGKLEIKGGGG 120  
 83 ESGVDPDRFGSGSGTDFLTISVQAEELAVYQNDSYPLTGAIGKLEIKGGGG 142

Db 121 GGSGGGGS-----EVQLEBQGAETVRPGTSVKTSCKSSQSLLNSNQKNTLYAWQPKGQSPKPLIYWASR 170

QY 143 KDAAKKDAAKKDAKKDALEQVQ-LOQSDAELVKGAVSKLSCASGYFTDHAIFWKQNP 201

Db 171 GHGLWIGDIFPGSGENIHYKHEKKAATLQDKSSSTAQNQSLTTERSAVFCARLEN 230

QY 202 RQGLWIGYFSPGNDPKYKWRKKGAKATLQDKSSSTAQNQSLTTERSAVFCARLEN 261

Db 231 WDEPMQDLYWQGCTTVTUSGGGS-----DIIKQSGAEJARPGAS 270

Db 262 --- MAYWQGQTSVTUSLSSADDAAKKDAKKDAKKDALEQVQLOQSDAELVKGAS 317

QY 271 VKMSCRTSGYFTTRYMHWTQRPQGQLENWGYINPSRGYTYNQKFQKATLTDKSS 330

RESULT 3  
 US-08-392-338A-19  
 ; Sequence 19, Application US/08392338A  
 ; Patient No. 5863620  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Whillow, Marc  
 ; APPLICANT: Wood, James F.  
 ; APPLICANT: Hardman, Karl  
 ; APPLICANT: Bird, Robert  
 ; APPLICANT: Filpila, David  
 TITLE OF INVENTION: Multivalent Antigen-Binding Protein  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Stern, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue, NW  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/392, 338A  
 FILING DATE: 22-FEB-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/989, 846  
 FILING DATE: 20-NOV-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796, 936  
 FILING DATE: 25-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REFERENCE/DOCKET NUMBER: 29, 021  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 483 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match  
 Best local Similarity 53.8%; Score 1283; DB 1; length 483;  
 Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELYWQPSLTLVTAEGKVTMSCKSSQSLLNSNQKNTLTWQPKGQSPKPLIYWASTR 60  
 1 DVMSQSPSILPVSVGKVKLTSCKSSQSLLNSNQKNTLYAWQPKGQSPKPLIYWASR 60

Db 61 ESGVDPDRFGSGSGTDFLTISVQAEELAVYQNDSYPLTGAIGKLEIKGGGG 120  
 61 ESGVDPDRFGSGSGTDFLTISVQAEELAVYQNDSYPLTGAIGKLEIKGGGG 119

QY 121 GGSGGGGS-----EVQLEBQGAETVRPGTSVKTSCKSSQSLLNSNQKNTLYAWQPKGQSPKPLIYWASR 180

Db 120 GKSSBGGQVQ-LOQSDAELVKGAVSKLSCASGYFTDHAIFWKQNP 178

QY 181 FPGSGNTHNEFKKGAKATLQDKSSSTAQNQSLTTERSAVFCARLENWDEPMQDLYWQGCTTVTUSGGGS 240

TYPE: amino acid  
 TOPOLGY: linear  
 MOLSCULE TYPE: protein  
 US-09-166-750-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
 Best Local Similarity 53.8%; Pred. No. 2.1e-87; Indels 132; Gaps 6;  
 Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 BLVMTQSPSNTVTAGEKVMSKCSQSLSNLSGNOKNLYWQQKPGQSPKL 294  
 Db 1 ILYWASAREGVPDFRGSGSGTDFTLS1SSVKTEDLAVYCCQOYYSYPLTFGAGTKVL 354  
 QY 295 ILYWASAREGVPDFRGSGSGTDFTLS1SSVKTEDLAVYCCQOYYSYPLTFGAGTKVL 354  
 QY 255 ----- -IKLQSGAELARGASVMSKCSQSLSNLSGNOKNLYWQQKPGQSPKL 298  
 QY 355 KSTSGSKSSEKGQVQLOQSDAELVKGASVKSCKASGYTFDTHHWKQNPBEGQI 414  
 Db 299 EMGYVNPNSRGYNTNQKFDKATLTDKSSSTAMQOSSLTSFEDSAVYCCARYDDYC 358  
 QY 415 EMGYFSFGNDDFKYNERFKGKATLTADKSSTAVYQNLTSFEDSAVYFCTRSLN--- 470  
 QY 359 LDYWGQGQSTLTVS 371  
 Db 471 MAYWGQGQSTLTVS 483

RESULT 4  
 US-09-166-750-19  
 Sequence 19, Application US/09166750  
 Patent No. 6021165

GENERAL INFORMATION:

APPLICANT: Whitolow, Marc  
 APPLICANT: Hardman, Karl  
 APPLICANT: Bird, Robert  
 APPLICANT: Filpula, David  
 APPLICANT: Rollence, Michelle

TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue, NW  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/166, 750  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/392, 338  
 FILING DATE: 22-FEB-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/989, 846  
 FILING DATE: 20-NOV-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796, 936  
 FILING DATE: 25-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29, 021  
 REFERENCE/DOCKET NUMBER: 0377.003000C

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2640

INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 483 amino acids

RESULT 4  
 US-09-166-750-19  
 Sequence 19, Application US/09166750  
 Patent No. 6021165

GENERAL INFORMATION:

APPLICANT: Whitolow, Marc  
 APPLICANT: Hardman, Karl  
 APPLICANT: Bird, Robert  
 APPLICANT: Filpula, David  
 APPLICANT: Rollence, Michelle

TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue, NW  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/166, 750  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/392, 338  
 FILING DATE: 22-FEB-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/989, 846  
 FILING DATE: 20-NOV-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796, 936  
 FILING DATE: 25-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29, 021  
 REFERENCE/DOCKET NUMBER: 0377.003000C

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2640

INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 483 amino acids

RESULT 5  
 US-09-166-093-19  
 Sequence 19, Application US/09166093  
 Patent No. 6027725

GENERAL INFORMATION:

APPLICANT: Whitolow, Marc  
 APPLICANT: Hardman, Karl  
 APPLICANT: Bird, Robert  
 APPLICANT: Filpula, David  
 APPLICANT: Rollence, Michelle

TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue, NW  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/166, 093

FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/392,338  
 FILING DATE: 22-FEB-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/989,846  
 FILING DATE: 20-NOV-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796,936  
 FILING DATE: 25-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29,021  
 REFERENCE/DOCKET NUMBER: 0977.003000B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 483 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-166-093-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
 Best Local Similarity 53.8%; Pred. No. 2.1e-87;  
 Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVMTQSSSLTTAGKUTMCKSSQSLIISNGNQKNLITWQOKPGQPPKKLIIWASTR 60  
 QY 1 DVMWSQSPSSLPVSVGEKVTLSCKSSQSLIISNGNQKNLAWYQOKPGQSPKKLIIWASAR 60  
 QY 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYVCONDYSPPLFGAGTKEIKGGGG 120  
 QY 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYVCONDYSPPLFGAGTKEIKGGGG 119  
 Db 121 GGSAGGGSEVQQLBQSGAELVPRGTSVKISCKSKASGYAFINYWLGWVKORPGHGLEWIGDI 180  
 QY 120 GKSSBKGQVQ-LQOSDAELVKPGASVKISCKSKASGYFTDHAHWWVKONPQEGLEWIGF 178  
 Db 181 FPGSGNIIHNEKFKGKATLTADKSSTAVQQLSLTFFSAVYCARLNRWDBPMYHQ 240  
 QY 179 SPGNDDFKNERFKKGKATLTADKSSTAVQQLSLTFFSAVYFCTRSLN---MAYWQ 234  
 Db 241 GTTVVSS----- 248  
 QY 235 GTSVTVSSDVMMSOSPSSLPVSVGEKVTLCKSSQSLIISNGNQKNLAWYQOKPGQSPKL 294  
 QY 249 -----GGGSD----- 254  
 Db 295 LIWASARESGVPDFRTGSGSGTDFLTISVQAEIDLAVYVCONDYSPPLFGAGTKEIKGGGG 354  
 QY 255 -----IKQSGAELVPRGTSVKISCKSKASGYFTDHAHWWVKONPQEGL 298  
 Db 355 KGSTSGSGKSSBKGQVQLOQOSDAELVKPGASVKISCKSKASGYFTDHAHWWVKONPQEGL 414  
 QY 299 EWIGYINPSRGYTNQKRDKAATLTADKSSTAVQQLSLTFFSAVYCARVYDHIC 358  
 Db 415 EWIGYFSPGNDDFKNERFKKGKATLTADKSSTAVQQLSLTFFSAVYFCTRSLN--- 470  
 QY 359 LDYQGQGTIVS 371  
 Db 471 MAYWQGTIVS 483

RESULT 6  
 US-09-172-019-19  
 Sequence 19 Application US/09172019  
 Patent No. 610389  
 GENERAL INFORMATION:  
 APPLICANT: Whitlow, Marc

APPLICANT: Hardman, Karl  
 APPLICANT: Bird, Robert  
 APPLICANT: Filpilia, David  
 TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
 TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Stern, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue, NW  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/172,019  
 FILING DATE: Herewith  
 ATTORNEY/AGENT INFORMATION:  
 APPLICATION NUMBER: US/09/172,019  
 FILING DATE: 22-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29,021  
 REFERENCE/DOCKET NUMBER: 0977.003000B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 483 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-172-019-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
 Best Local Similarity 53.8%; Pred. No. 2.1e-87;  
 Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVMTQSSSLTTAGKUTMCKSSQSLIISNGNQKNLITWQOKPGQPPKKLIIWASTR 60  
 QY 1 DVMWSQSPSSLPVSVGEKVTLSCKSSQSLIISNGNQKNLAWYQOKPGQSPKKLIIWASAR 60  
 QY 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYVCONDYSPPLFGAGTKEIKGGGG 120  
 QY 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYVCONDYSPPLFGAGTKEIKGGGG 119  
 Db 121 GGSAGGGSEVQQLBQSGAELVPRGTSVKISCKSKASGYAFINYWLGWVKORPGHGLEWIGDI 180  
 QY 120 GKSSBKGQVQ-LQOSDAELVKPGASVKISCKSKASGYFTDHAHWWVKONPQEGLEWIGF 178  
 Db 181 FPGSGNIIHNEKFKGKATLTADKSSTAVQQLSLTFFSAVYCARLNRWDBPMYHQ 240  
 QY 179 SPGNDDFKNERFKKGKATLTADKSSTAVQQLSLTFFSAVYFCTRSLN---MAYWQ 234  
 QY 241 GTTVVSS----- 248  
 Db 235 GTSVTVSSDVMMSOSPSSLPVSVGEKVTLCKSSQSLIISNGNQKNLAWYQOKPGQSPKL 294  
 QY 249 -----GGGSD----- 254  
 Db 295 LIWASARESGVPDFRTGSGSGTDFLTISVQAEIDLAVYVCONDYSPPLFGAGTKEIKGGGG 354



PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796, 936  
 FILING DATE: 25-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29,021  
 REFERENCE/DOCKET NUMBER: 0977.003000E  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 483 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-443-213-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
 Best Local Similarity 53.8%; Pred. No. 2.1e-87; Mismatches 37; Indels 132; Gaps 6;  
 Matches 265; Conservative

QY 1 BLVMTQSPSLLTVAKEKTMCKSSQSLLNSGNQKNLTYWQKPGQPPKLLIYASTR 60  
 Db 1 DVMQSQSPSLLPVSGEKVTLCKSSQSLLSGNQKNLTYWQKPGQPPKLLIYASTR 60  
 QY 61 ESGVYDRAFTGSGSDFTLTISSVQAOEADLAVYVCONDYSYPLTFAGTKLEIKGGGG 120  
 Db 61 ESGVYDRAFTGSGSDFTLTISSVQTKEDLAVYVQQYISYPLTFAGTKLKLK-GSTSGS 119

QY 121 GSGSGGGSVQULLRSGAELVRPCTSVKCKASGYAFTNYMIGWVKORGHGLEMIDI 180  
 Db 120 GKSBBGKGQVO-LOQSDAELVKPGASKVSKASGYFTDHAHWVKONPQGLEWICP 178

QY 181 FPGSONIHTBKPKKATLTADKSSTAYVQLNLSITFEDSAVFCARLNWDEPMYMQ 240  
 Db 179 SGNDPFKYNERFKKATLTADKSSTAYVQLNLSITFEDSAVFCARLNWDEPMYMQ 234

QY 241 GTTVTVSS----- 248

Db 235 GSTVTVSSDVMMSQSPSSLPVSGEKVTLCKSSQSLLSGNQKNLTYWQKPGQSPKLU 294

QY 249 -----GGGGSD----- 254

Db 295 LIYIWA8ARESGVPDFRFTGSGSDFTLTISSVQTKEDLAVYVQQYISYPLTFAGTKLVL 354

QY 255 -----IKLQSGAELAROQASVMSCKTSGYFTTRYHEWVKORGQOL 298

Db 355 KGSTSGSGKSESGKGQVOQLOQSDAELVKPGASKVSKCKASGYFTDHAHWVKONPDEGL 414

QY 299 FHWIGVYNPSRGYTNQNKFKKATLTADKSSTAYVQLNLSITFEDSAVFCARYDDHYC 358

Db 415 EwigfFSPGNDPFKYNERFKKATLTADKSSTAYVQLNLSITFEDSAVFCARLN----- 470

QY 359 LDYNGQGTTVVS 371

Db 471 MAYWQGQGTSVTVS 483

RESULT 9  
 US-08-263-911-7  
 Sequence 7, Application US/08263911  
 Patent No. 5877291  
 GENERAL INFORMATION:  
 APPLICANT: Meze, Peter S  
 APPLICANT: Gourlie, Brian B  
 TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 STREET: P. O. Box 1967  
 CITY: Midland  
 STATE: MI

COUNTRY: US  
 ZIP: 48641-1967  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/263, 911  
 FILING DATE: 21-JUN-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/990, 263  
 FILING DATE: 11-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ulmer, Duane C  
 REGISTRATION NUMBER: 34,941  
 REFERENCE/DOCKET NUMBER: C-41, 014  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 636-8104  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 553 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 23

US-08-263-911-7

Query Match 60.1%; Score 1230.5; DB 1; Length 553;  
 Best Local Similarity 48.3%; Pred. No. 1.9e-83; Mismatches 37; Indels 177; Gaps 6;  
 Matches 261; Conservative

QY 1 BLVMTQSPSLLTVAKEKTMCKSSQSLLNSGNQKNLTYWQKPGQPPKLLIYASTR 60  
 Db 23 DVMQSQSPSLLPVSGEKVTLCKSSQSLLSGNQKNLTYWQKPGQPPKLLIYASTR 60  
 QY 61 ESGVYDRAFTGSGSDFTLTISSVQTKEDLAVYVQQYISYPLTFAGTKLKLK-GSTSGS 120

Db 83 ESGVYDRAFTGSGSDFTLTISSVQTKEDLAVYVQQYISYPLTFAGTKLKLK-SADDK 142

QY 121 GSGGGGGS-----EVOLLEQSGAELVRGTSVYKCKASGYAFTNYMIGWVKORG 170  
 Db 143 KDAAKKDDAKKDDAKKDDLKVQ-LOQSDAELVKPGASKVSKCKASGYFTDHAHWVKONP 201

QY 171 GHGLEWID31FPGSGNINIIINNEKFKKATLTADKSSTAYVQLNLSITFEDSAVFCARLN 230

Db 202 EGGEWIG3YFSPGNDPFKYNERFKKATLTADKSSTAYVQLNLSITFEDSAVFCARLN 261

QY 231 WDEPMYQGTTVVS----- 248

Db 262 -----MAYWQGQGTSVTVS 254

QY 249 -----GGGGSD----- 254

Db 318 KVTLCKSSQSLLSGNQKNLTYWQKPGQSPKLUWASARESGVPDFRFTGSGSDFT 377

QY 255 ----- 254

Db 378 TLSISSVQTKEDLAVYVQQYISYPLTFAGTKLVLKLSADDAKKDAAKKDDAKKDD 437

QY 255 --IKLQSGAELAROQASVMSCKTSGYFTTRYHEWVKORGQOL 312

Db 438 LEVOLQSDAELVKPGASKVSKCKASGYFTDHAHWVKONPQGQLEBINGYFSPGNDPFK 497

QY 313 YNQFKDKKATLTADKSSTAYVQLNLSITFEDSAVFCARYDDHYCILYWGQGTITVSS 372

Db 498 YNERFPKATLTADKSSTAYVQLNLSITFEDSAVFCARLN-----MAYWQGQGTSVTVS 553

RESULT 10







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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:22 ; Search time 25 seconds (without alignments)  
 1454.797 Million cell updates/sec

**Title:** US-10-743-697-1  
**Perfect score:** 2046  
**Sequence:** IELVMTQSPSPLITVAGEKVT.....IDYWGQGTTLTVSSHHHHH 378

**Scoring table:** BLOSUM62  
**Gapop:** 10.0 , Gapext 0.5

**Searched:** 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

**Post-processing:** Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

**Database :** PIR\_80;\*  
 1: pir1;\*  
 2: pir2;\*  
 3: pir3;\*  
 4: pir4;\*

**pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match length	DB	ID	Description
1	631	30.8	287	4	PC4402	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
2	576	28.2	113	2	PL0263	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
3	563.9	27.5	220	2	A31790	C;Species: synthetic
4	548	26.8	112	2	F30538	C;Accession: PC4402 C;Species: synthetic C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998 R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T. J. Biochem. 122, 322-329, 1997 A;Title: Construction, bacterial expression, and characterization of hapten-specific antibodies A;Reference number: PC4402
5	545	26.6	112	2	B30538	A;Accession: PC4402 A;Molecule type: DNA A;Residues: 1-287 <SUS> A;Cross-references: UNIPARC:UPI000017CF08 C;Keywords: fusion protein
6	539	26.3	113	2	PL0264	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
7	532	26.0	108	2	E30535	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
8	532	26.0	135	2	S38807	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
9	530.5	25.9	139	2	PS0024	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
10	527	25.8	107	2	G30535	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
11	524	25.6	107	2	F30535	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
12	520	25.4	107	2	D30535	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
13	512	25.0	268	2	A56446	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
14	507	24.8	105	2	C30535	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
15	507	24.8	140	2	PH1489	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
16	503	24.6	113	2	A49260	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
17	502.5	24.6	118	2	PR0356	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
18	502.5	24.6	139	2	A27609	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
20	500	24.4	140	1	HYN5G7	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
21	499.5	24.4	120	2	S41394	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
22	499.5	24.4	131	2	S66533	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
23	499.5	24.4	249	2	S41374	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
24	497.5	24.3	138	2	S20404	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
25	496	24.2	145	2	PL0263	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
26	495.5	24.2	112	2	PL0265	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
27	495.5	24.2	214	2	S88212	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
28	494.5	24.2	240	2	S06084	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
29	494	24.1	140	2	PH1489	pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -

**RESULT 1**

Query Match 30.8%; Score 631; DB 4; length 287;  
 Best Local Similarity 52.5%; Pred. No. 1-6e-33; Mismatches 78; Indels 22; Gaps 6; Matches 138; Conservative 25; Mismatches 78; Indels 22; Gaps 6; Matches 138; Conservative 25; Mismatches 78; Indels 22; Gaps 6;

QY 1 ELVMTQSPSPLITVAGEKVTMSCKSSOSLNSGNQKNVLYQDKPGQPRPKLILWASTER 60  
 Dp 26 QAVVTOE SALVTTSPGETVLTCTCSSTGAVTT--SNVANVWQEKEDHIFTGLIGETNRR 81

QY 61 ESGVYDRAFTGSGSGTDFITIISVQAEQDILAVYCONDYSVPLTCAGTKLEI----- 112  
 Dp 82 APGVAPRSGSLIGDKAALITITQAGTEDAIVYRGLWVSNHWVFGGTKLTVLSSADAK 141

QY 113 -----KG3GSGSGGSGGGSEVOLQEDQGAEYLPGTSVKSICKASGYVFTNYWGMWV 167  
 Dp 142 KDDAKKDDAKKDDAKKDG---QVO-LQQKAEELVKGASVSKLSCASGIFTSYMMHWV 197

QY 168 QRPQHGLEIITDIFPGSGMHNHYNEKFKGKATLADKSSAYMQLSSTEDSAYVFCAR 227  
 Dp 198 QRPQHGLEIITDIFPGSGMHNHYNEKFKGKATLADKSSAYMQLSSTEDSAYVFCAR 257

QY 228 LRNNDEP-MDYWGQGTIVTWSGG 249  
 Dp 258 YDYIGSSYFDYWGQGTIVTWSGG 280

**ALIGNMENTS**

A;Molecule type: mRNA  
 A;Residues: 1-113 <SHL>  
 A;Cross-references: UNIPARC:UPI000176AF7  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-23/Region: framework 1  
 F;16-96/Domain: immunoglobulin homology <IMM>  
 F;24-40/Region: complementarity-determining 1  
 F;56-62/Region: framework 2  
 F;63-94/Region: complementarity-determining 2  
 F;95-103/Region: framework 3  
 F;104-113/Region: complementarity-determining 3  
 F;104-113/Region: framework 4

Query Match 28.2%; Score 576; DB 2; Length 113;  
 Best Local Similarity 95.5%; Pred. No. 1.9e-30; Matches 109; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 A;Reference number: F30534; MUID:89035545; PMID:3141511

Qy 1 BLVMTQSPLTIVTAGKVYTMCKSSQSLLNSGNOKNLTWYQOKPGQPPKKLIYMASTER 60  
 1 DIVMTQSPSLLTIVTAGKVYTMCKSSQSLLNSGNOKNLTWYQOKPGQPPKKLIYMASTER 60

Db 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 113  
 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 113

RESULT 3

A31790 Ig kappa chain V region (17/9) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Accession: A31790 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
 R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
 J. Biol. Chem. 263, 17100-17105, 1988  
 A;Title: Preliminary crystallographic data, primary sequence, and binding data for an arabinose-binding protein.  
 A;Reference number: A92686; MUID:89034213; PMID:3182835  
 A;Accession: A31790  
 A;Molecule type: mRNA  
 A;Residues: 1-20 <SCH>  
 A;Cross-references: UNIPARC:UPI0000114E12; GB:W03626; GB:J04061; NID:9533234; PIDN:AA319  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 27.5%; Score 563.5%; DB 2; Length 220;  
 Best Local Similarity 52.3%; Pred. No. 5.5e-29; Matches 123; Conservative 19; Mismatches 48; Indels 45; Gaps 5;  
 A;Reference number: F30538; MUID:89035545; PMID:3141511

Qy 1 BLVMTQSPLTIVTAGKVYTMCKSSQSLLNSGNOKNLTWYQOKPGQPPKKLIYMASTER 60  
 1 DIVMTQSPSLLTIVTAGKVYTMCKSSQSLLNSGNOKNLTWYQOKPGQPPKKLIYMASTER 60

Db 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 120  
 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 113

RESULT 4

F30538 Ig kappa chain V region (253-15D10) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Accession: F30538 #sequence\_revision 10-Feb-1989 #text\_change 21-Jan-2000  
 C;Keywords: heterotetramer; immunoglobulin  
 R;Clafelin, J.L.; Berry, J.

Qy 181 PPGSGNIHY---NSFKFKGKATLADK-SSSTAYMQLSSIT----FEDSAVYRC 225  
 146 YPKDINWKWDGSRQNGVLSWQDQSKDSTVMSMSTLTKEYERHNNSYRC 200

Db 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 180  
 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 145

RESULT 5

BB0538 Ig kappa chain V region (253-12D3) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Accession: BB0538 #sequence\_revision 10-Feb-1989 #text\_change 21-Jan-2000  
 R;Clafelin, J.L.; Berry, J.  
 J;Immunol. 141, 4012-4019, 1988  
 A;Title: Genetics of the phosphocholine-specific antibody response to *Streptococcus pneumoniae*  
 A;Reference number: A30534; MUID:89035545; PMID:3141511  
 A;Accession: BB0538  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-112 <CLA>  
 A;Cross-references: UNIPARC:UPI000176CD4  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 26.8%; Score 548; DB 2; Length 112;  
 Best Local Similarity 92.9%; Pred. No. 1.1e-28; Matches 104; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 BLVMTQSPLTIVTAGKVYTMCKSSQSLLNSGNOKNLTWYQOKPGQPPKKLIYMASTER 60  
 1 DIVMTQSPSLLSVAQEYVMTCKSSQSLLNSGNOKNLTWYQOKPGQPPKKLIYMASTER 60

Db 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 112  
 61 ESGVDRFTGSGSGTDFLTISVQAEIDLAVYYCQNDISYPLTFGAGKLEIK 112

RESULT 6

PL0264 Ig kappa chain V region (anti-DNA, D20VK) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Accession: PL0264 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marchak-Rothstein, A.  
 J. Exp. Med. 171, 265-297, 1990  
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic recombination  
 A;Reference number: PL0231; MUID:90111618; PMID:2104919  
 A;Accession: PL0264  
 A;Molecule type: mRNA  
 A;Residues: 1-113 <SHL>  
 A;Cross-references: UNIPARC:UPI000176AFB  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin

R;Clafelin, J.L.; Berry, J.

F;1-23/Region: framework 1  
 F;6-96/Domain: immunoglobulin homology <IMM>  
 F;24-40/Region: complementarity-determining 1  
 F;41-55/Region: framework 2  
 F;56-62/Region: complementarity-determining 2  
 F;63-94/Region: framework 3  
 F;95-103/Region: complementarity-determining 3  
 F;104-113/Region: framework 4

Query Match 26.3%; Score 539; DB 2; Length 113;  
 Best Local Similarity 91.2%; Pred. No. 4.4e-28; Indels 0; Gaps 0;  
 Matches 103; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSTIVTAGEKVITMSCKSSQSLNSQNLWYQOKPGQPPLKLYWASTR 60  
 DB 1 DIVMTQSPSLSVSAKGKVNMSCKSSQSLNSQNLWYQOKPGQPPLKLYGASTR 60

QY 61 ESGVDPDRFTGSGSGIDFTLTISSVQAEGLAVVYCONDYSPLTGAGTKLKI 113  
 DB 61 ESGVDPDRFTGSGSGIDFTLTISSVQAEGLAVVYCONDYSPLTGAGTKLKI 113

RESULT 7  
 E30335  
 Ig kappa chain V region (6D10) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 23-Feb-1989 #sequence\_revision 23-Feb-1989 #text\_change 21-Jan-2000  
 C;Accession: E30535  
 R;Clafin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.  
 J. Immunol. 138, 3060-3068, 1987  
 A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with  
 A;Reference number: A30556; MUID:87196439; PMID:3106498  
 A;Accession: E30535  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-108 <CL>  
 A;Cross-references: UNIPARC:UPI0000176AED  
 A;Note: the sequence was determined from the differentiated gene  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 26.0%; Score 532; DB 2; Length 108;  
 Best Local Similarity 93.5%; Pred. No. 1.2e-27; Indels 0; Gaps 0;  
 Matches 101; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSTIVTAGEKVITMSCKSSQSLNSQNLWYQOKPGQPPLKLYASTR 60  
 DB 1 DIVMTQSPSLSVSAKGKVNMSCKSSQSLNSQNLWYQOKPGQPPLKLYGASTR 60

QY 61 ESGVDPDRFTGSGSGIDFTLTISSVQAEGLAVVYCONDYSPLTGAGT 108  
 DB 61 ESGVDPDRFTGSGSGIDFTLTISSVQAEGLAVVYCONDYSPLTGAGT 108

RESULT 8  
 S38807  
 Ig light chain V-J region - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C;Accession: S38807  
 R;Sequeira, A.; Avraneas, S.; Jouvain-Marche, E.  
 Immunogenetics 36, 15-21, 1992  
 A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2  
 A;Reference number: S38807; MUID:9226756; PMID:1587549  
 A;Accession: S38807  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-135 <SEQ>  
 A;Cross-references: UNIPARC:UPI0000176CA6; EMBL:X59816  
 A;Note: the authors translated the codon GGC for residue 1 as Ala and TGT for residue 21  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: immunoglobulin

RESULT 9  
 PS0024  
 Ig heavy chain precursor V region (6A1) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 22-Nov-1996  
 C;Accession: PS0024  
 R;Marget, M.; Ehrhart, A.; Ehret, W.; von Specht, B.U.; Duchen, M.; Domdey, H.  
 Gene 74, 335-345, 1988  
 A;Title: Cloning and characterization of cDNAs coding for the heavy and light chains of  
 A;Reference number: PS0023; MUID:89232725; PMID:314994  
 A;Accession: PS0024  
 A;Molecule type: mRNA  
 A;Residues: 1-139 <MAR>  
 A;Cross-references: UNIPARC:UPI0000176D41  
 A;Experimental source: strain BALB/C  
 C;Comment: This chain is obtained from an IgG2a monoclonal antibody against *Pseudomonas*  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-113/Domain: Ig heavy chain V region #status predicted <IGV>  
 F;34-117/Domain: immunoglobulin homology <IMM>  
 F;20/Modified Site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted  
 Query Match 25.9%; Score 530.5; DB 2; Length 119;  
 Best Local Similarity 79.4%; Pred. No. 1.9e-27; Indels 1; Gaps 1;  
 Matches 100; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 248 SGGGGSDIKLQOSGAFELARPGASVKNQCKSGTSGYFTTYMEWKQKPGQGLEWIGYINPS 307  
 DB 14 TAGVHSQVQLQSGASGAIKPGASVKNQCKSGYFTYMEWKQKPGQGLEWIGYINP 73

QY 308 RGYTNNTQKEDKATLTDKESSTAYNQLSLTSITSDAVYCAR YYDDHYCLDWGQGT 366  
 DB 74 TGYTEYNQFKDQKATLADKSSTAYNQLSLTSEDAVYCTRSYVNEYGAMDYNGQT 133

QY 367 TLTVSS 372  
 DB 134 SVTVSS 139

RESULT 10  
 G30535  
 Ig kappa chain V region (2G6) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Accession: G30535  
 R;Clafin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.  
 J. Immunol. 138, 3061-3068, 1987  
 A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with  
 A;Reference number: A30556; MUID:87196439; PMID:3106498  
 A;Accession: G30535  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-107 <CL>  
 A;Cross-references: UNIPARC:UPI0000176AF6  
 A;Note: the sequence was determined from the differentiated gene  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin

F;16-96/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 25.8%; Score 527; DB 2; Length 107;

Best Local Similarity 93.5%; Pred. No. 2.4e-27; Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 BLVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: UNIPARC:UPI0000176AF9

Db 1 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

RESULT 11

Ig kappa chain V region (5G4) - mouse (fragment)

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

RESULT 12

Ig kappa chain V region (5G4) - mouse (fragment)

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Species: Mus musculus (house mouse) C;Cross-references: F30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

RESULT 13

Ig kappa chain V region (5C8) - mouse (fragment)

C;Species: Mus musculus (house mouse) C;Cross-references: B30535

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Accession: B30535

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

R;Clafelin, J. L.; Berry, J.; Flaherty, D.; Dunnick, W. J. Immunol. 138, 3060-3068, 1987

A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A;Reference number: AJ0556; MUID:87196439; PMID:3106498

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-107 <CLA>

A;Cross-references: UNIPARC:UPI0000176AF5

A;Note: the sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-96/Domain: immunoglobulin homology <IMM>

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-107 <CLA>

A;Cross-references: UNIPARC:UPI0000176AF5

A;Note: the sequence was determined from the differentiated gene C;Keywords: heterotetramer; immunoglobulin C;Key words: heterotetramer; immunoglobulin

A;Accession: B30535

QY 61 ESGVPDFRTGSGSGTDFITLITISSVQAEDLAVYVQNDVSYPLTFGAG 107

RESULT 14

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C;Species: Mus musculus (house mouse) C;Cross-references: A56446

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

C;Accession: A56446

R;Mang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A. J. Biol. Chem. 270, 7429-7435, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical A;Reference number: AJ6446; MUID:95229583; PMID:7713873

A;Status: preliminary

A;Molecule type: RNA

A;Residues: 1-268 <TA>

A;Cross-references: UNIPARC:UPI0000176CD0; GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 512; DB 2; Length 268;

Best Local Similarity 42.6%; Pred. No. 6.1e-26; Matches 115; Conservative 45; Mismatches 62; Indels 48; Gaps 11;

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 133 LEQSGAELVPGTSVSKICKASGAYFMYLGMKQRCGHLGEWIGDIFPGSGNTHMEK 192

Db 61 DIVMTQSSSLTVAGEKUTMSCKSSQSLNSNQKVLTWYQOKPGQPPKLLYMASTER 60

QY 193 FKGATLADKSSTAYMQLSLSTFEDAVYCAVYVTRYE--NYGQGTRTVSSGG 247

Db 66 FQGRATIADTSSTAYMQLSLSTFEDAVYCAVYVTRYE--NYGQGTRTVSSGG 122

Db 248 -----SAGGGSPIKQDQGAGL-ARGASVSKCK-TSGYFPTRYHWWKQRPQGCL 298

Db 123 GGSQGDDSGEGGSPIELTQSPATMSASGEKVTMSCRASSSVF---IYIQQKSDASP 178

RESULT 15  
C30535

Ig kappa chain V region (2B2) - mouse (fragment)  
C.Species: *Mus musculus* (house mouse)  
C.Date: 23-Feb-1989 #sequence\_revision 23-Feb-1989 #text\_change 21-Jan-2000  
C.Accession: C3D533

J. Immunol. 138, 3060-3068, 1987  
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with  
A;Reference number: A30556; MUID:87196439; PMID:106498  
A;Accession: C30536  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-105 <CL4>  
A;Cross references: UNIPARC:UPI000176AF4  
A;Note: the sequence was determined from the differentiated gene  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query	Match	24.8%	Score	507	DB	2	Length	105
Best	Local	Similarity	90.5%	Pred.	No.	4.5e-26		
Matches	95;	Conservative	7;	Mismatches	3;	Indels	0;	Gaps
Oy	1	BLUMTQSPSSLJUTVAGKRVUMCKSSQSLNSNGQKNYLTWYQOKPGQPKPLLTWASTR					60	
Db	1	DIUMTQSPSSLVSAGKXVMSCKSSQSLNSNGQKNYLTWYQOKPGQPKPLLTGASTR					60	
QY	61	ESGVPDFRTGSGSGTDFLTISQAEGLAVYCONDYSPLTG	105					
Db	61	ESGVPDFRTGSGSGTDFLTIVSVAQEDBLAVYYCQNDHTYPLTRG	105					

Search completed: March 6, 2006, 13:14:48  
Job time : 26 secs

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Db	RESULT 2	175 SITGGYMWIRKFFGKNDYMGYI-NYSGDTYNNPLKERSITADTSRNQYVQQLQNSVT 233
Ov	Q7TQM2_MOUSE PRELIMINARY;	PRT; 243 AA.
Db	Q7TQM2;	
AC	01-OCT-2003 (TREMBrel. 25, Created)	
DT	01-OCT-2003 (TREMBrel. 25, Last sequence update)	
DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)	
DR	Se-Fv_6H8 protein (Fragment).	
GN	Name=Se-Fv_6H8;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.	
OC	NCBI_TaxID=10090;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=Balb/c;	
RA	Peter J.C., Wallukat G., Tugluer J., Maurice D., Roegel J.C.,	
RA	Briand J.P., Hoebeke J.;	
RT	Modulation of the M2 muscarinic acetylcholine receptor activity with monoclonal anti-M2 receptor antibody fragments.;	
RL	J. Biol. Chem. 279:55697-55706 (2004).	
DR	EMBL: AJ46180; CAA34081.1; -; Other_DNA.	
DR	HSSP: P01337; IgCR.	
DR	InterPro: IPR03559;	
DR	InterPro: IPR007110; Ig-like.	
DR	InterPro: IPR03590; Ig_V.	
DR	SMART: SNO409; Ig; 2.	
DR	SMART; SNO406; Ig_V; 2.	
DR	PROSITE; PS50835; Ig_LIKE; 2.	
FT	NON_TER 1 1	
SQ	SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;	
Query Match	27.7%; Score 566; DB 2; Length 243;	
Best Local Similarity	90.3%; Pred. No. 1.9e-34;	
Matches	124; Conservative 33; Mismatches 71; Indels 36; Gaps 9;	
RT	"IgV single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	
RL	J. Biol. Chem. 278:36740-36747 (2003).	
DR	EMBL: AU574851; CAB04955.1; -; Genomic_DNA.	
DR	HSSP; P01751; IgW.	
DR	SMR; Q7TQM2; 1-236.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR03596; Ig_V.	
DR	SMART; SNO406; Ig_V; 2.	
DR	PROSITE; PS50835; Ig_LIKE; 2.	
FT	NON_TER 1 1	
SQ	SEQUENCE 243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;	
Query Match	27.7%; Score 566; DB 2; Length 243;	
Best Local Similarity	90.3%; Pred. No. 1.5e-31;	
Matches	102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	
RT	"IgV single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	
RL	J. Biol. Chem. 278:36740-36747 (2003).	
DR	EMBL: AU574851; CAB04955.1; -; Genomic_DNA.	
DR	HSSP; P01751; IgW.	
DR	SMR; Q7TQM2; 1-236.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR03596; Ig_V.	
DR	SMART; SNO406; Ig_V; 2.	
DR	PROSITE; PS50835; Ig_LIKE; 2.	
FT	NON_TER 1 1	
SQ	SEQUENCE 243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;	
Query Match	27.7%; Score 566; DB 2; Length 243;	
Best Local Similarity	90.3%; Pred. No. 1.5e-31;	
Matches	102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	
RT	"IgV single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	
RL	J. Biol. Chem. 278:36740-36747 (2003).	
DR	EMBL: AU574851; CAB04955.1; -; Genomic_DNA.	
DR	HSSP; P01751; IgW.	
DR	SMR; Q7TQM2; 1-236.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR03596; Ig_V.	
DR	SMART; SNO406; Ig_V; 2.	
DR	PROSITE; PS50835; Ig_LIKE; 2.	
FT	NON_TER 1 1	
SQ	SEQUENCE 243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;	
Query Match	27.7%; Score 566; DB 2; Length 243;	
Best Local Similarity	90.3%; Pred. No. 1.5e-31;	
Matches	102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	
RT	"IgV single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	
RL	J. Biol. Chem. 278:36740-36747 (2003).	
DR	EMBL: AU574851; CAB04955.1; -; Genomic_DNA.	
DR	HSSP; P01751; IgW.	
DR	SMR; Q7TQM2; 1-236.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR03596; Ig_V.	
DR	SMART; SNO406; Ig_V; 2.	
DR	PROSITE; PS50835; Ig_LIKE; 2.	
FT	NON_TER 1 1	
SQ	SEQUENCE 243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;	
Query Match	27.7%; Score 566; DB 2; Length 243;	
Best Local Similarity	90.3%; Pred. No. 1.5e-31;	
Matches	102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	
RT	"IgV single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	
RL	J. Biol. Chem. 278:36740-36747 (2003).	
DR	EMBL: AU574851; CAB04955.1; -; Genomic_DNA.	
DR	HSSP; P01751; IgW.	
DR	SMR; Q7TQM2; 1-236.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR03596; Ig_V.	
DR	SMART; SNO406; Ig_V; 2.	
DR	PROSITE; PS50835; Ig_LIKE; 2.	
FT	NON_TER 1 1	
SQ	SEQUENCE 119 AA; 13567 MW; BAB93873FD5F6AB CRC64;	
Query Match	25.8%; Score 527; DB 2; Length 119;	
Best Local Similarity	78.8%; Pred. No. 6.8e-32;	
Matches	93; Conservative 12; Mismatches 13; Indels 0; Gaps 0;	
RT	"IgV single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	
RL	J. Biol. Chem. 278:36740-36747 (2003).	
DR	EMBL: AF282622; AAG1452.1; -; mRNA.	
DR	HSSP; P01751; IgW.	
DR	SMR; Q7TQM2; 1-236.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR03596; Ig_V.	
DR	SMART; SNO406; Ig_V; 2.	
DR	PROSITE; PS50835; Ig_LIKE; 1.	
FT	NON_TER 1 1	
SQ	SEQUENCE 119 AA; 13567 MW; BAB93873FD5F6AB CRC64;	
Query Match	25.8%; Score 527; DB 2; Length 119;	
Best Local Similarity	78.8%; Pred. No. 6.8e-32;	
Matches	93; Conservative 12; Mismatches 13; Indels 0; Gaps 0;	

QY	255	IKLQSQGELARPGASVSKMCKTSQGTYFTRYTMWVQKRPQGLEWIGYINPNSRGYTN	052L2 9MURI
Db	2	:VOLVSGAEVKRPKGASVRYSKASQYTFQGYMMWVQKRPQGLEWIGYINPNSRGYTN	052L2 9MURI PRELIMINARY; PRT; 487 AA.
QY	315	QKFQDKATLTTDKSSSTAVMQLSSITSEDSAVVYCARYYDDHYCLDYNGQGTIVS	052L2; 61
Db	62	QKFQDKATLTTDKSSSTAVMQLSSITSEDSAVVYCARYYDDHYCLDYNGQGTIVS	052L2; 61
RESULT	5	Q4KML5_MOUSE PRELIMINARY;	052L2; 61
ID	Q4KML5	PRTR; 617 AA.	AC
AC	Q4KML5_		Q52L2;
DT	13-SEP-2005	(TREMBrel. 31, Created)	DT
DT	13-SEP-2005	(TREMBrel. 31, Last sequence update)	DT
DT	13-SEP-2005	(TREMBrel. 31, Last annotation update)	DT
DE	Hypothetical protein.		DE
OS	Mus musculus (Mouse)		FV/M4.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		Name=M4-IFN-<tau>;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		Mus sp.
OC	Mammalia; Muridae; Murinae; Mus.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Muridae; Muridae; Murinae; Mus.		Mammalia; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;		NCBI_TaxID=10095;
RN	[1]		[1]
RP	NUCLEOTIDE SEQUENCE.		NUCLEOTIDE SOURCE.
RC	STRAIN=57BL/6NC;		NUCLEOTIDE SOURCE.
RX	MEIDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;		Qi Y., Xiang J.;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		"A genetically engineered single-gene-encoded anti-TAG72 chimeric antibody secreted from myeloma cells";
RA	Klaunser R.D., Collins F.S., Wagner L., Sheehan C.M., Schuler G.D.,		Hum. Antibodies Hybridsomas 6:161-166 (1995).
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		EMBL; S8249; AAB7442; - mRNA.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		DR; GO; GO:0003823; F antigen binding; IEA.
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		DR; InterPro; IPR031598; Ig; Ig-like.
RA	Stapleton M., Soares M.B., Bandallo M.F., Casavant T.L., Scheetz T.B.,		DR; InterPro; IPR031598; Ig; Ig c1.
RA	Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,		DR; InterPro; IPR031598; Ig; Ig c2.
RA	Raha S.S., Louellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		DR; InterPro; IPR031598; Ig; Ig MHC.
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,		DR; InterPro; IPR031598; Ig; Ig V.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		DR; InterPro; IPR031598; Ig; Ig set 2.
RA	Villalon D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,		DR; SMART; SM00407; IgC1; 2.
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		DR; SMART; SM00408; IgC2; 2.
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		DR; SMART; SM00405; IgV; 2.
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		DR; SMART; SM00406; IgV; 2.
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.B.,		DR; PROSITE; PS00353; Ig; Ig-like; 4.
RA	Butterfield Y.S.N., Krzyniak M.I., Skalska U., Smailus D.E.,		DR; PROSITE; PS00290; Ig MHC; 1.
RA	Schernch A., Schein J.E., Jones S.J.M., Marra M.A.,		DR; SEQUENCE; 487 AA; 53578 MW; C7BAB69F30555504 CRC64;
RT	"Generation and initial analysis of more than 15,000 full-length human		Query Match 25.3%; Score 518; DB 2; Length 487;
RL	and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		Best Local Similarity 46.2%; Pred. No. 1. 8e-30; Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
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RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
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RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
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RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTP		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTX		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTN		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA	BLASTR		Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;
RA			

OC Muroidea; Muridae; Murinae; Mus.  
 OX NOBI\_TAXID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MIX FVB/N;  
 RX TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 MEDLINE=23308257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.J., Wagner D., Schaefer C.F., Bhat N.K.,  
 RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muniz D.M., Soderberg B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Heitton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherzer A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MIX FVB/N;  
 RX TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RG NIH MGC Project;  
 RG Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC094049; DAH94049.1; -; mRNA.  
 DR InterPro: IPR003595; Ig.  
 DR SMART: S00407; IgCl; 1.  
 DR SMART: S00406; IgV; 1.  
 DR PROSITE: PS50835; Ig\_LIKE; 2.  
 DR PROSITE: PS00290; Ig\_MHC; UNKNOWN\_1.  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 240 AA; 26609 MW; CT8630CCC002B52C CRC64;  
 Query Match 24.9%; Score 508.5; DB 2; Length 240;  
 Best Local Similarity 47.7%; Pred. No. 4e-30;  
 Matches 112; Conservative 26; Mismatches 52; Indels 45; Gaps 5;  
 QY 1 BLWMTQSPSLITVAGEKVWMSCKSQQSLNSIGNRKNLYTWYQQKPGQPQPKLTYWASTR 60  
 QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 21 DIVMSQSPSSLAVSVEKTYMSCKSQQSLNSIGNRKNLYTWYQQKPGQPQPKLTYWASTR 80  
 Db 61 ESGVDFRGSGSGTDTLTTISVQARDLAVYYCONDYKPLTQAGTKEIKGGSGG 120  
 Db 81 ESGVDFHFSGGSGTDTLTTISVQARDLAVYYCONDYKPLTQAGTKEIKGGSGG 133  
 QY 121 GGGGGGGSEVOLLESGAELVRPGTSVKTSCKASQYAPTMWLGWVQKRGHGLWIGDI 180  
 Db 134 --RADAAPTVSIFPPSSEOLTSQGGSV-----VCFLNPF 165  
 QY 181 FPGSGNIHY---NIRFKGKQTLTADK-SGSTMQQLSSIT----FEDAVYFC 225  
 Db 166 YPKDINVKWKGDSRQNGVLSWTDQDSKDSVTSMSSTLTQDVEYRHNSYTC 220  
 RESULT 8  
 Q569W9\_MOUSE  
 ID Q569W9\_MOUSE PRELIMINARY; PRT; 468 AA.  
 QY 243 TTVVSSGGGSDIKLQSGAELARP-----GASVMSCKTSQYIFTTRYTMHWVQR 293

AC Q569W9;  
 DT 10-MAY-2005 (TREMBLrel. 30, Created)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=Igh-1a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarctontogires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 RN NOBI\_TAXID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZECH II;  
 RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
 MEDLINE=23308257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner D., Shehman C.M., Schuler G.D.,  
 RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherzer A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZECH II;  
 RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
 RG NIH MGC Project;  
 RG Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC092271; DAH92271.1; -; mRNA.  
 DR SMR: Q569W9; 20-64.  
 DR MGI: MGI:96443; Igh-1a.  
 DR GO: GO:0008283; F antigen binding; IHA.  
 DR InterPro: IPR003595; Ig.  
 DR InterPro: IPR003199; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003586; Ig\_V.  
 DR Pfam: PF07654; Cl-set; 1.  
 DR SMART: S00405; Ig; 2.  
 DR SMART: S00407; IgCl; 1.  
 DR SMART: S00406; IgV; 1.  
 DR PROSITE: PS50835; Ig\_LIKE; 2.  
 DR PROSITE: PS00290; Ig\_MHC; UNKNOWN\_1.  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 240 AA; 26609 MW; CT8630CCC002B52C CRC64;  
 Query Match 24.9%; Score 508.5; DB 2; Length 240;  
 Best Local Similarity 53.0%; Pred. No. 3e-29; Matches 53; Indels 19; Gaps 3;  
 Matches 105; Conservative 21; Mismatches 53; Indels 19; Gaps 3;  
 QY 123 SGCGGGSEVOLLESGAELVRPGTSVKTSCKASQYAPTMWLGWVQKRGHGLWIGDFF 182  
 QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 14 TAGVSEVO-LOQSGAELVRPGTSVKTSCKASQYAPTMWLGWVQKRGHGLWIGDFF 72  
 Db 183 GSGNHYNIRFKGKQTLTADK-SGSTMQQLSSITFEDAVYFC 242  
 Db 73 GNGTYEVNKEFKGKQTLTADK-SGSTMQQLSSITFEDAVYFC 132





Best Local Similarity	75.6%	Pred. No.	3.5e-28	DR	PIR; PH1153; PH1153.		
Matches	96;	Conservative	11;	HSSP;	P01751; IAW.		
		Mismatches	16;	DR	SMR; Q924R0; 1-134.		
		Indels	4;	DR	InterPro; IPR007110; Ig-like.		
		Gaps	2;	DR	InterPro; IPR00396; Ig_v.		
QY	122	GSGGGSEVOLLEGSGAELVRPGTSVSKCASKASYFTMYWLGWVKQRPQHGLBWWGDF	181	DR	SMART; SMO0406; IgV; 1.		
	13	GTAGVHQCQQLKQSGAELVPGASKLUSCKASCGYFTFTDYYINWKQRPQHGLBWWGDF	181	DR	PROSITE; PSS0835; Ig_LIKE; 1.		
Db	182	PGSGNIHYMEKKKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLIRNDEPDHYWGCG	241	FT	NON_TER 1		
QY	72	PGSGTYTNEKKKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLIRNDEPDHYWGCG	128	FT	NON_TER 143 143		
Db	242	TVTVVSS 248	135	SQ	SEQUENCE 143 AA; 15868 MW; 139B2P966B81E07F CRC64;		
QY	129	TSVTVSS		Query Match	23.8%; Score 486.5; DB 2; Length 143;		
Db	129	TSVTVSS	135	Best Local Similarity	76.3%; Pred. No. 9.5e-29; DR		
		Matches	90;	Matches	90; Conservative 13; Mismatches 14;		
		Indels	1;	Gaps	1;		
RESULT	13	Q924R0_MOUSE PRELIMINARY	PRT;	143 AA.	DR		
ID	Q924R0;	01-DEC-2001 (TREMBIxel. 19, Created)	AC	255 IKLQOOGABTLARPGASVSKMSCKTSGYFTFTDYYINWKQRPQHGLBWWGDF	314		
DT	01-DEC-2001 (TREMBIxel. 19, Last sequence update)	DT	01-DEC-2001 (TREMBIxel. 19, Last sequence update)	DR	2 VOLQPGAAELVKPGASKVSKCASKASYFTSYWMEVKQRPQHGLBWWGDF		
OX	NCBI_TAXID=10090;	OX	01-OCT-2003 (TREMBIxel. 25, Last annotation update)	DR	62 EFKSKATLVDKPSSTAYMQLSSLTSEDSAVYFCAR-NDEDYAMDYNGQTSVVS	118	
RN	[1]	NUCLEOTIDE SEQUENCE.	GN	Name=AB069917; Synonyms=v23-D-J-C mu;	OS		
RC	STRAIN=C57BL/6;	RC	Mus musculus (Mouse);	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RA	Kozono Y., Kozono H., Azuma T.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.	OC	Mammalia; Buteraria; Euarchontoglires; Glires; Rodentia; Sciuromathi;	OC	Mammalia; Buteraria; Euarchontoglires; Glires; Rodentia; Sciuromathi;		
RL	[2]	Mus musculus (Mouse);	OC	Muridae; Murinae; Mus.	OC	Muridae; Murinae; Mus.	
RN	Pubmed=3135311;	DR	Corbet S., Hirn M., Roth C., Theze J., Fougerneau M., Schiff C.; Immunization of	DR	Corbet S., Hirn M., Roth C., Theze J., Fougerneau M., Schiff C.; Immunization of	DR	Corbet S., Hirn M., Roth C., Theze J., Fougerneau M., Schiff C.; Immunization of
RA	Corbet S., Hirn M., Roth C., Theze J., Fougerneau M., Schiff C.; Immunization of	DR	"Allogeneic manipulation of the GAT idiotypic cascade. Immunization of	DR	"Allogeneic manipulation of the GAT idiotypic cascade. Immunization of	DR	"Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT	"Allogeneic manipulation of the GAT idiotypic cascade. Immunization of	DR	C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-	DR	C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-	DR	C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	specific V genes as the original antigen.,"; Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).	DR	specific V genes as the original antigen.,"; Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).	DR	specific V genes as the original antigen.,"; Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	J. Immunol. 141:779-784 (1988).	DR	J. Immunol. 141:779-784 (1988).	DR	J. Immunol. 141:779-784 (1988).
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	EMBL; AB067790; BAB3275.1, -; mRNA.	DR	EMBL; AB067790; BAB3275.1, -; mRNA.	DR	EMBL; AB067790; BAB3275.1, -; mRNA.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; F28833; F28833.	DR	PIR; F28833; F28833.	DR	PIR; F28833; F28833.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; F33932; F33932.	DR	PIR; F33932; F33932.	DR	PIR; F33932; F33932.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1105; PH1105.	DR	PIR; PH1105; PH1105.	DR	PIR; PH1105; PH1105.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1108; PH1108.	DR	PIR; PH1108; PH1108.	DR	PIR; PH1108; PH1108.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1114; PH1114.	DR	PIR; PH1114; PH1114.	DR	PIR; PH1114; PH1114.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1118; PH1118.	DR	PIR; PH1118; PH1118.	DR	PIR; PH1118; PH1118.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1119; PH1119.	DR	PIR; PH1119; PH1119.	DR	PIR; PH1119; PH1119.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1125; PH1125.	DR	PIR; PH1125; PH1125.	DR	PIR; PH1125; PH1125.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1126; PH1126.	DR	PIR; PH1126; PH1126.	DR	PIR; PH1126; PH1126.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1128; PH1128.	DR	PIR; PH1128; PH1128.	DR	PIR; PH1128; PH1128.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1129; PH1129.	DR	PIR; PH1129; PH1129.	DR	PIR; PH1129; PH1129.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1131; PH1131.	DR	PIR; PH1131; PH1131.	DR	PIR; PH1131; PH1131.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1134; PH1134.	DR	PIR; PH1134; PH1134.	DR	PIR; PH1134; PH1134.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1137; PH1137.	DR	PIR; PH1137; PH1137.	DR	PIR; PH1137; PH1137.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1139; PH1139.	DR	PIR; PH1139; PH1139.	DR	PIR; PH1139; PH1139.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1142; PH1142.	DR	PIR; PH1142; PH1142.	DR	PIR; PH1142; PH1142.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1144; PH1144.	DR	PIR; PH1144; PH1144.	DR	PIR; PH1144; PH1144.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1147; PH1147.	DR	PIR; PH1147; PH1147.	DR	PIR; PH1147; PH1147.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1149; PH1149.	DR	PIR; PH1149; PH1149.	DR	PIR; PH1149; PH1149.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1150; PH1150.	DR	PIR; PH1150; PH1150.	DR	PIR; PH1150; PH1150.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1151; PH1151.	DR	PIR; PH1151; PH1151.	DR	PIR; PH1151; PH1151.
RT	"Two murine natural polyreactive autoantibodies are encoded by	DR	PIR; PH1152; PH1152.	DR	PIR; PH1152; PH1152.	DR	PIR; PH1152; PH1152.
Query Match	23.7%	Score	485;	DB	2; length 140;		
Best Local Similarity	78.8%	Pred. No.	1.2e-28	DR	HSSP; P01751; IAW.		
Matches	93;	Conservative	6;	DR	SMR; Q924R0; 1-134.		
QY	255	IKLQOOGABTLARPGASVSKMSCKTSGYFTFTDYYINWKQRPQHGLBWWGDF	314	DR	InterPro; IPR007110; Ig-like.		
Db	2	VQLQPGAAELVKPGASKVSKCASKASYFTSYWMEVKQRPQHGLBWWGDF	61	DR	InterPro; IPR00396; Ig_v.		



Thu Mar 9 15:13:59 2006

us-10-743-697-1.rup

Page 9

Db ||||: |||: |||: |||: |||:  
133 LYTIVSAAKTAPSVYPLAPVCGGT-----TGSStvTUGCLVKGyFEPVTLW 179  
QY |||:  
290 VKQRPQGQLEWIGYINPSRCYTYTNQNQFKDKATLTD 326  
Db |||:  
180 MSGLSSGVHTPPALQSGIYT----LSSSVTIVSN 211

Search completed: March 6, 2006, 14:48:20  
Job time : 113 secs

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OM protein - protein search, using SW model

Run on: March 6, 2006, 13:20:36 ; Search time 35 Seconds (without alignments)  
 216.005 Million cell updates/sec

Scoring table: BiOSSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 2000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA\_New:\*

1: /cgn2\_6/podata/2/pubpaa/US08\_NEW\_PUB.pep:\*

2: /cgn2\_6/podata/2/pubpaa/US06\_NEW\_PUB.pep:\*

3: /cgn2\_6/podata/2/pubpaa/US07\_NEW\_PUB.pep:\*

4: /cgn2\_6/podata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

5: /cgn2\_6/podata/2/pubpaa/US09\_NEW\_PUB.pep:\*

6: /cgn2\_6/podata/2/pubpaa/US10\_NEW\_PUB.pep:\*

7: /cgn2\_6/podata/2/pubpaa/US11\_NEW\_PUB.pep:\*

8: /cgn2\_6/podata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1  
 US-10-495-664-3  
 Sequence 3 Application US/10495664  
 Publication No. US2005024416A1  
 GENERAL INFORMATION:  
 APPLICANT: JUNG, GUNDRAM  
 TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODIES  
 FILE REFERENCE: 03:258-0801  
 CURRENT APPLICATION NUMBER: US/10/495,664  
 CURRENT FILING DATE: 2004-05-12  
 PRIOR APPLICATION NUMBER: PCT/EP02/12545  
 PRIOR FILING DATE: 2002-11-09  
 PRIOR APPLICATION NUMBER: DE 101 56 482.1  
 PRIOR FILING DATE: 2001-11-12  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn Ver. 3.3  
 SEQ ID NO 3  
 LENGTH: 543  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence  
 OTHER INFORMATION: protein construct  
 US-10-495-664-3  
 Query Match 55.3%; Score 1130.5; DB=2.2e-64  
 Best Local Similarity 56.7%; Pred. No. 2.2e-64  
 Matches 224; Conservative 59; Mismatches 8  
 Qy 1 ELWMTQSPSLTVAGEKVT...  
 21 DIVLQTPSPASLAVSLQGATRISCRASEV...-EY  
 Db 21  
 Qy 57 ASTRESGVPPRTFGSGGSDPTLTSSVQADLVY  
 135 GGGGGGGGGGGGGSGVK-LQOSGPGLVTPSLSLIC  
 Db 75 ASNTESGVPARFESSGGSGTFLSNLHPVDDVAMYF  
 Qy 176 WIGDIPFGSGSNIHMKFKKATLADKSSTAYM  
 116 GGGGGGGGGGGSEVQLEGGSGAELVYRPGPSVKISCK  
 194 WLGVWAGGETNYSNALSMSRKSKISDNKSKQVFLK  
 Db 135 GGGGGGGGGGGGGSGVK-LQOSGPGLVTPSLSLIC  
 Qy 234 PMDYKQGTTTWS-----SGGGSDIK  
 253 SMDYKQGTTWVSSASTKPSVFLPAPSSGGQKRT  
 Db

## SUMMARIES

is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

Copyright (c) 1993 - 2006 GenCore version 0.9.1  
 OM protein - protein search, using SW model  
 Run on: March 6, 2006, 13:20:36 ; Session 2  
 Title: US-10-743-697-1  
 Perfect score: 2046  
 Sequence: 1 ELVMTQSPSSLIVTVAEKGVT.....  
 Scoring table: BL2USUMG2  
 Gapop 10.0 , Gapext 0.5  
 Searched: 135346 seqs, 2000420 residues  
 Total number of hits satisfying chosen parameters: 2

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**OM protein - protein search, using sw model**

Run on: March 6, 2006, 13:20:36 ; Search time 35 Secors  
 (without alignments) 216.005 Million cells

Title: US-10-743-697-1  
 Perfect score: 2046  
 Sequence: I ELVMTIQSPSSLTVTVAEKT . . . . . LDYWGQGTTLTIVSSH

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen Parameters: 135346

**Copyright (c) 1993 - 2006 Biocceleration Ltd.**  
**GenCore version 5.1.7**  
**OM protein - protein search, using sw model**  
**Run on:** March 6, 2006, 13:20:35 ; **Search time 35 Seconds**  
**(without alignments)**  
**Title:** US-10-743-697-1  
**Perfect Score:** 2046  
**Sequence:** 1 ELVMTQFSSSLVTVAGEKVT. .... 135346 seqs, 20000420 residues  
**Scoring table:** BLOSUM62  
**Searched:** Gapop 10.0 , Gapext 0.5  
**Total number of hits satisfying chosen parameters:** 135346

Copyright (c) 1993 - 2006 Biocceleration Ltd.  
**Om protein - protein search, using sw model**

Run on: March 6, 2006, 13:20:36 ; Search time 35 Seconds  
 (without alignments)  
 216.005 Million cell updates/sec

Title: US-10-743-697-1  
 Perfect score: 2046  
 Sequence: 1 ELVMTQSFSSLTVTAGEKVT..... LDYNGQGTLTLTVSSHHHHH 378

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 135345 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

**GenCore** version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: March 6, 2006, 13:20:36 ; Search time 35 Seconds  
 (without alignments)  
 216.005 Million cell updates/sec  
 Title: US-10-743-697-1  
 Perfect score: 2046  
 Sequence: 1 ELWMTQSPSLITVAGEKVT. .... LDYWGQGTTLTVSSHHHHH 378  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 135346 seqs, 2000420 residues  
 Total number of hits satisfying chosen parameters: 135346

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 6, 2006, 13:20:36 : Search time 35 Seconds  
 (without alignments)  
 216.005 Million cell updates/sec

Title: US-10-743-697-1

Perfect score: 2046

Sequence: 1 ELVMTQSPSLTIVAGEKVT. .... LDYWGQGTTLVSSHHHHH 378

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 2000420 residues

Total number of hits satisfying chosen parameters: 133346

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**GenCore version 5.1.7**  
**Om protein - protein search, using sw model**  
**Run on:** March 6, 2006, 13:20:35 ; **Search time 35 Seconds**  
**(without alignments)**  
**216.005 Million cell updates/sec**  
**Title:** US-10-743-697-1  
**Perfect Score:** 2046  
**Sequence:** 1 ELVMTQSFSSLTVTAGERKVT. .... . LDYWGQGTLTLTVSSHHHHH 378  
**Scoring table:** BL05M62  
**Gapop 10.0 , Gapext 0.5**  
**Searched:** 135346 seqs, 20000420 residues  
**Total number of hits satisfying chosen parameters:** 135346  
27 612.5 29.9 226 7 US-11-183-205  
28 609.5 29.8 6 US-10-512-184  
29 602 29.9 6 US-10-512-184  
30 600 29.3 290 7 US-11-032-773  
31 585.5 28.6 319 7 US-11-032-773  
32 562.5 27.5 248 6 US-10-512-184  
33 558 27.3 113 7 US-11-076-395  
34 553 27.0 113 7 US-11-076-395  
35 533 26.1 241 6 US-10-512-546  
36 529.5 25.9 249 7 US-11-201-825  
37 529.5 25.9 277 7 US-11-126-817  
38 528.5 25.8 277 7 US-11-126-817  
39 527 25.8 113 7 US-11-076-395  
40 526.5 25.7 248 6 US-10-512-184  
41 524 25.6 252 7 US-11-054-512  
42 525 25.5 328 7 US-11-079-907  
43 521 25.5 263 6 US-10-512-184  
44 519 25.4 119 7 US-11-221-900  
45 519 25.4 119 7 US-11-221-900

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GenCore version 5.1.7

Om protein - protein search, using sw model

Run on: March 6, 2006, 13:20:35 ; Search time 35 Seconds  
(without alignments)

216.005 Million cell updates/sec

Title: US-10-743-697-1

Perfect Score: 2046

Sequence: 1 ELVMTQSFSSLTVTAGERKVT. .... LDYWGQGTLTLVSSHHHHH 378

Scoring table: BL05M62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

27 612.5 29.9 226 7 US-11-183-205-42 Sequence

28 609.5 29.8 6 US-10-512-184-69 Sequence

29 602 29.4 6 US-10-512-184-50 Sequence

30 600 29.3 7 US-11-032-773-957 Sequence

31 585.5 28.6 7 US-11-032-773-955 Sequence

32 562.5 27.5 7 US-10-512-184-32 Sequence

33 558 27.3 7 US-11-076-395-46 Sequence

34 553 27.0 7 US-11-076-395-45 Sequence

35 533 26.1 6 US-10-512-184-6 Sequence

36 529.5 25.9 7 US-11-201-825-24 Sequence

37 529.5 25.9 7 US-11-126-817-52 Sequence

38 528.5 25.8 7 US-11-126-817-54 Sequence

39 527 25.8 7 US-11-076-395-16 Sequence

40 526.5 25.7 6 US-10-512-184-36 Sequence

41 524 25.6 7 US-11-054-515-157 Sequence

42 525 25.5 7 US-11-079-907-4 Sequence

43 521 25.5 6 US-10-512-184-29 Sequence

44 519 25.4 7 US-11-221-900-13 Sequence

45 519 25.4 7 US-11-221-900-14 Sequence

QY 280 YIFTRYTMWYKQRGQGLEWIGYNNPNSRGTYNNQKFQDATTUDKESSTAYMQLSSL 339  
Db 313 YAFSRSMWNVKQRGQGLEWIGYNNPNSRGTYNNQKFQDATTUDKESSTAYMQLSSL 372  
Db 340 TSBDSSAVVYCAR--YDDHYCLDYWGQGTTLTVSS 372  
Db 373 TSVDSSAVVFCARGNTVVVWYPTMDYWGQGTTTVSS 407

RESULT 2

US-11-116-939-11

Sequence 11, Application US/11116939  
Publication No. US20050265995A1

GENERAL INFORMATION:

APPLICANT: Stephen Tomlinson

APPLICANT: Richard J. Quiggy

TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS

FILE REFERENCE: 19113.0115U2

CURRENT APPLICATION NUMBER: US/11/116,939

CURRENT FILING DATE: 2005-04-28

PRIOR APPLICATION NUMBER: 60/565,907

PRIOR FILING DATE: 2004-04-28

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 824

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence; note=synthetic

OTHER INFORMATION: construct

US-11-116-939-11

RESULT 2  
US-11-116-939-11  
; Sequence 11, Application US/1116939  
Qy 280 YTFRYTMHVKQKRGQGLEIYGTPRSQGYTNNQKFKEK  
Db 313 YAFSRWMWVKQKPGGLEWIGTRYPGDGTNYNGKFR  
Qy 340 TSESSAVYCAR - YDDHKCLDMQGOTLTIVS 3722  
Db 373 TSVDSAVYFCARGNTVWVPTYMDWQGQGTTVVS 4077

PRIOR APPLICATION NUMBER: 60/565,907  
PRIOR FILING DATE: 2004-04-28  
NUMBER OF SEQ ID NOS: 27  
SEQUENCE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 412  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
OTHER INFORMATION: construct  
US-11-116-939-12

QY 280 YTFRTRTMWIKQRPQGQLEWIGYINPSPREYTNQKFDKATTTDKESSTAMQISSLSS  
Db 313 YAFSRMRNWWYKRPQGQLEWIGYIYPGDDETNQKFKGKATTTDKESSTAMQISSLSS  
Db 340 TSEDASVYCAR--YVDDHKLDDYNGQGTTVSS 372  
Db 373 TSVDSAVYFCARGNTVWVPTMDYNGQGTTVSS 407

RESULT 2

US-11-116-939-11

Sequence 11, Application US/11116939

Publication No. US2005026595A1

GENERAL INFORMATION:

APPLICANT: Stephen Tomlinson

APPLICANT: Richard J. Quig

TITLE OF INVENTION: TISSUE TARGETTED COMPLEMENT MODULATORS

FILE REFERENCE: 19113\_011512

CURRENT APPLICATION NUMBER: US/11/116,939

CURRENT FILING DATE: 2005-04-28

PRIOR APPLICATION NUMBER: 60/565,907

PRIOR FILING DATE: 2004-04-28

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 824

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
OTHER INFORMATION: construct

US-11-116-939-11

RESULT 2  
US-11-116-939-11  
Sequence 11, Application US/11116939  
Publication No. US20050265995A1  
GENERAL INFORMATION:  
APPLICANT: Stephen Tomlinson  
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS  
FILE REFERENCE: 19113.0115U2  
CURRENT APPLICATION NUMBER: US/11/116, 939  
PRIORITY APPLICATION NUMBER: 60/565, 907  
PRIORITY FILING DATE: 2005-04-28  
NUMBER OF SEQ ID NOS: 27  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 12  
LENGTH: 412  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
US-11-116-939-12  
Sequence 12, Application US/11116939  
Publication No. US20050265995A1  
GENERAL INFORMATION:  
APPLICANT: Stephen Tomlinson  
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS  
FILE REFERENCE: 19113.0115U2  
CURRENT APPLICATION NUMBER: US/11/116, 939  
PRIORITY APPLICATION NUMBER: 60/565, 907  
PRIORITY FILING DATE: 2005-04-28  
NUMBER OF SEQ ID NOS: 27  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 11  
LENGTH: 824  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
US-11-116-939-11  
Query Match 48.5%; Score 992; DB 7; Length 412;  
Best Local Similarity 65.5%; Bred. No. 8.6e-56; Mismatches 41; Indels 42; Gaps 6;  
Matches 203; Conservative 24; Mismatches 41; Indels 42; Gaps 6;  
QY 1 BLVMTQSPSSITIVAGBKVTMSCKSQSOSLNSGNGNQKNTWYQKRSQCPPLKLIVASTR 60  
Db 25 DIVMQQPSLAVSVGEKVMTNCKSSQL--KTNQKNLYAWYQKQGOSPLKLIVASSR 82  
QY 61 BSGVDRFTGSGSGTDTLTTSSVQEDLAVYYCNDYSVPLTFFGAGTKLRLKGGGG 120  
Db 83 ESGVFDRTGSGSGTDTLTTSSVQEDLAVYYCNDYSVPLTFFGAGTKLRLKGGGG 142  
QY 121 GGSGGGGGSMGWSVCMVFLPLVATATGVHSQVO-LEOSPELVPGVSKICKSGYIFTDY 161  
Db 143 GGSGGGGGSMGWSVCMVFLPLVATATGVHSQVO-LEOSPELVPGVSKICKSGYIFTDY 201  
QY 162 WLGWIKQRPQHGLEWIGDIFPGSGNHINHNSKFKGKATLADKSSTAYMQQSLTEDSA 221  
Db 202 AHWYKQSHAKSLBMLWIGVISTYYGKHYNGKFKGKATLTVKSSNTAYMELRILTSEDA 261  
QY 222 VYCARLNNMB---PMDWQGJTTVTSGGGGSDIKLQQSGAELARPGAVK--- 272  
Db 262 IYCARPNNGSSSPPYTAMDWGQGTSVTSGGGG---SGGGGSGGGSLRCYNC 314  
QY 273 ---MSCKTS 278  
Db 315 DDPVSSCKTN 324  
RESULT 4  
US-11-116-939-10  
Sequence 10, Application US/11116939  
Publication No. US20050265995A1  
GENERAL INFORMATION:  
APPLICANT: Stephen Tomlinson  
APPLICANT: Richard J. Quigg  
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS  
FILE REFERENCE: 19113.0115U2  
CURRENT APPLICATION NUMBER: US/11/116, 939  
PRIORITY APPLICATION NUMBER: 60/565, 907  
PRIORITY FILING DATE: 2005-04-28  
NUMBER OF SEQ ID NOS: 27  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 10  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
US-11-116-939-10  
RESULT 3  
US-11-116-939-12  
Sequence 12, Application US/11116939

QY 280 YTPTRYTHWYKQKRPQGLEMWGYINPREGTYNNQKFQDQKATLTIDESSTAYMQSSL 339  
 Db 313 YAFSRSMWNVKQGPQGLEWGRYRPGDQNTNGKFKATLTIDESSTAMQVSL 372  
 QY 340 TSBD5AVVYCAR--YDDHYCLDWGQGTTLVSS 372  
 Db 373 TSVD5AVVFCARGNTVVPYTMQWQGCTVTSS 407

RESULT 2  
 US-11-116-939-11  
 Sequence 11, Application US/11116939  
 Publication No. US20050265995A1  
 GENERAL INFORMATION:  
 APPLICANT: Stephen Tomlinson  
 APPLICANT: Richard J. Quigg  
 TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS  
 FILE REFERENCE: 19113.0115U2  
 CURRENT APPLICATION NUMBER: US/11/116, 939  
 CURRENT FILING DATE: 2005-04-28  
 PRIORITY APPLICATION NUMBER: 60/565, 907  
 PRIORITY FILING DATE: 2004-04-28  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 11  
 LENGTH: 824  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence; note=synthetic  
 OTHER INFORMATION: Construct  
 US-11-116-939-12

Query Match 48.5%; Score 992; DB 7; Length 412;  
 Best Local Similarity 65.5%; Pred. No. 8.6-56; Mismatches 41; Indels 42; Gaps 6;  
 Matches 203; Conservative 24; Mismatches 41; Indels 42; Gaps 6;  
 QY 1 BLVMTQSPSSITIVTAGKVNTMSKSSQSLSANGNOKNLYTQQKQCPQPPKLIYAWSTR 60  
 Db 25 DIVMSQSPSSLAWSVGEKVNMCKSSQSL--KTNQKNLYAWQKRGQSPKPLIYAWSSR 82

QY 61 RSGVDRFTGSGGMDFTLTSSQADELAVYVQNDYSPFLTGFAGTKLKEIKGGSGG 120  
 Db 83 ESGVDRFTGSGGMDFTLTSSQADELAVYVQDQYSPLTGFAGTKLKEIKGGSGG 142

QY 121 GGGGGGG-----SEVOLBQSGAELVRPGTSVKSICRASGYFTNY 161  
 Db 143 GGGGGGSGMGSCVMLPLVATATGHSQVQ-LEQSPELVPGVSKISCKSGYFTDY 201

QY 162 WGMWYKQRPQHGLEMWDIPGSGNHYNRFKQKATLTAKSSSTAYMOSSLTEDSA 221  
 Db 202 AHWYKQSHAKSLWENLWIGVISTYYGHTHONRQFKGKATLTWVKSNTAYMELARTSEDSA 261

Db 25 DIVMSQSPSSLAVSVGEKVYMMCKSQSL--KTNQKNYIAWYQDQKPGQSPKLILYWASSR 82

Qy 61 ESGVPDFRGSGSGTDFLTISVQADELAVVYCONDYSYPLIFGAGTKLEIKGGGGGG 120

Db 83 BSGVPDFRGSGSGTDFLTISVQADELAVVYCONDYSYPLIFGAGTKLEIKGGGGGG 142

Qy 121 GSGGGGG-----SEVOLLSQSGAELVRPGTSVKISCKASQAFNTY 161

Db 143 GSGGGGGSGWCSYMLFLVATATGVHSQVQ-LEOSGPFLVRPGVSVKISCKGGSGTFDY 201

Qy 162 WLGNWIKQPOHGLEWIGDIFPPGSGNHYNEFKKGKATLTADKSSTAYMQLSSTPESA 221

Db 202 AHWYKQSHAKSLMENIGVISTYQGHTHVNQFKKGKATLTADKSSTAYMQLSSTPESA 261

Qy 222 VYFCARLRNWDB----PMDWGQGTIVTWS 248

Db 262 IYCARPNNYGSSPPYIAMDQCGQTSVTVS 293

RESULT 5

US-10-981-356A-29

; Sequence 29, Application US/10981356A

; Publication No. US200501552A1

; GENERAL INFORMATION:

; APPLICANT: FILVAROFF, ELLEN H.

; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT

; FILE REFERENCE: P2063R1

; CURRENT APPLICATION NUMBER: US/10/981,356A

; CURRENT FILING DATE: 2004-11-04

; PRIOR APPLICATION NUMBER: US 60/520,398

; PRIOR FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: US 60/557,951

; PRIOR FILING DATE: 2004-03-31

; NUMBER OF SEQ ID NOS: 45

; SEQ ID NO 29

; LENGTH: 666

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: sequence is synthesized

; OTHER INFORMATION: Unsure

; LOCATION: 220

; OTHER INFORMATION: Unknown amino acid

; US-11-096-046-29

Query Match 46.5%; Score 952; DB 6; Length 666;

Best Local Similarity 55.4%; Pred. No. 4.2e-53; Indels 46; Gaps 10; Matches 209; Conservative 36; Mismatches 86;

Query Match 46.1%; Score 942.5; DB 7; Length 667;

Best Local Similarity 55.3%; Pred. No. 1.7e-52; Indels 47; Gaps 11; Matches 209; Conservative 37; Mismatches 85;

Db 1 ELMVTOQPSSTIVTNGBKVTSCKSSQSLNSGNQKNLYTWYQKQGQPPKLLIYASTER 60

Qy 1 DIMITTQPSSSLAVSAGKVKVTSCKSSQSLNSGNQKNLYTWYQKQGQPPKLLIYASTER 60

Db 61 ESGVPDFRGSGSGTDFLTISVQADELAVVYCONDYSYPLIFGAGTKLEIKGGGGGG 120

Qy 61 ESGVPDFRGSGSGTDFLTISVQADELAVVYCONDYSYPLIFGAGTKLEIKGGGGGG 120

Db 61 ESGVPDFRGSGSGTDFLTISVQADELAVVYCONDYSYPLIFGAGTKLEIKGGGGGG 112

Qy 121 GSGGGGSEVOLQSGAELVRPGTSVKISCKASQAFNTYWLGNWIKQRGHGLBWIWGI 180

Db 113 --RTVAAPSVFIPPSDEQL-KSGTA-SVVC----LLNNFYPREAK----VQWVVDN 157

Qy 181 FPGSGNHYNEFKKGKATLTADKSSTAYMQLSST-----FEDSAVYFCARLNWDEPM 235

Db 158 ALQSGN-----SOSVTPQSKDSTYSLSTLSDTAKSDYKHKVYAC-----EV 201

Qy 236 DWGQGTIVTWS-SGGGSDIKLQSGAELARPGAVSKMSCKTSGYTFTRYTMHWKQRP 294

Db 202 THQGLSSPVTKSFRGECXEVQLOQSGAELVRPGTSVKISCKASQAFNTYIEWKQRP 261

Qy 295 GQGLEWIGYINPSRGYTYNQKFDKATLTADKSSTAYMQLSSTEDSAYVARYDD 354

Db 262 GQGLEWIGVNNPGGGGSYNEFKKGKATLTADKSSTAYMQLSSTEDSAYVFCAR--S 319

Qy 181 FPGSGNHYNEFKKGKATLTADKSSTAYMQLSST-----FEDSAVYFCARLNWDEPM 235

Db 158 ALQSGN-----SOSVTPQSKDSTYSLSTLSDTAKSDYKHKVYAC-----EV 201

Qy 236 DWGQGTIVTWS-SGGGSDIKLQSGAELARPGAVSKMSCKTSGYTFTRYTMHWKQRP 295

Db 202 THQGLSSPVTKSFRGECXEVQLOQSGAELVRPGTSVKISCKASQAFNTYIEWKQRP 261

RESULT 7

US-11-084-717-21

; Sequence 21, Application US/11084717

; Publication No. US20050260766A1

; GENERAL INFORMATION:

; APPLICANT: GEORGIOT, GEORGE

; APPLICANT: JEONG, KI-TUN

; APPLICANT: HARVEY, BARRETT R.

Qy 295 QGLEWIGYINPSRGYTYNQKFDKATLTADKSSTAYMQLSSTEDSAYVARYDD 355

Db 262 QGLEWIGVNNPGGGGSYNEFKKGKATLTADKSSTAYMQLSSTEDSAYVFCAR--S 319

Qy 356 HYCLDYGQGTIVTWS 372

Db 320 GQFVFDWQGQTSVTVS 336





RESULT 14  
US-11-179-244-25

; OTHER INFORMATION: Peptide  
US-11-084-055B-25

Query Match 40.3%; Score 825.5; DB 7; Length 247;  
Best Local Similarity 63.4%; Pred. No. 1.6e-45;  
Matches 161; Conservative 32; Mismatches 48; Indels 13; Gaps 3;  
QY 1 ELVMTQSPSLIVTAGEKVTMCKSSQSLNSGNOKNLTWYQQKPGQPPKLLIWASTR 60  
Db 1 DIQWQTQITSSLASIGDRVIVTSCRASQD-----RNLYWQKRPDGTVKFLIYVTSRL 54  
QY 61 ESGVDRFCGSGSPDTLWISSVAEDLAVVYCONDSPLTFCAGTKEIK-----G 114  
Db 55 LPGVPSRFSGSGSDYSLTINNLEQBDIGTYFCQGNIPFWFOGGTKEIKRGGGSD 114  
QY 115 GGGSGGGSGGGSEVOLIQLQSGAELVRLPETSVKISCKSKASGYAFPNWIGWVKORPGHGL 174  
Db 115 GGGSGGGSGGGSEVQ-LOQSGPVELVKPGASKVSKCKSKOSGYAFNNSWWMKVKORPGQL 173  
QY 175 EWIGDTFPGSNIHYNNEKFKGKATLTADKESSTAYMQLSITFEDSAVFCARLRNWDEP 234  
Db 174 EWIGRIYFGDGSNITKGPKEGKAILTADKESSTAYMQLSITFEDSAVFCARSGILLRYA 233  
QY 235 MDYWGQGTIVVSS 248  
Db 234 MDYWGQGTIVVSS 247

Search completed: March 6, 2006, 13:22:29  
Job time : 35 secs

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OM protein - protein search, using SW model

Run on: March 6, 2006, 13:19:02 ; Search time 80 Seconds  
 (without alignments)  
 1974.244 Million cell updates/sec

Title: US-10-743-697-1  
 Perfect score: 2046  
 Sequence: ELYNTQSPLSLTVTAGKVT.....LDYWGQGTLTVSSHRRHHHH 378

scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA\_Main:\*

1: /cgn2\_6/pctodata/1/pupbaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/pctodata/1/pupbaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/pctodata/1/pupbaa/US10\_PUBCOMB.pep:\*

4: /cgn2\_6/pctodata/1/pupbaa/US10\_PUBCOMB.pep:\*

5: /cgn2\_6/pctodata/1/pupbaa/US11\_PUBCOMB.pep:\*

6: /cgn2\_6/pctodata/1/pupbaa/US11\_PUBCOMB.pep:\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Length	DB	ID	Description
1	2046	100.0	378	5	US-10-743-697-1	Sequence 1, Appli
2	1484.5	72.6	495	3	US-09-940-004-18	Sequence 18, Appli
3	1484.5	72.6	495	5	US-10-672-932-18	Sequence 18, Appli
4	1476	71.7	500	4	US-10-162-809-22	Sequence 22, Appli
5	1439.5	70.4	499	5	US-10-177-111	Sequence 111, Appli
6	1414	69.1	492	4	US-10-682-845-59	Sequence 59, Appli
7	1409	68.9	492	4	US-10-682-845-61	Sequence 61, Appli
8	1407	68.8	492	4	US-10-682-845-87	Sequence 87, Appli
9	1406	68.7	492	4	US-10-682-845-65	Sequence 65, Appli
10	1406	68.7	492	4	US-10-682-845-67	Sequence 67, Appli
11	1405	68.7	492	4	US-10-682-845-63	Sequence 63, Appli
12	1405	68.7	492	4	US-10-682-845-71	Sequence 71, Appli
13	1404	68.6	492	4	US-10-682-845-69	Sequence 69, Appli
14	1401	68.5	492	4	US-10-682-845-73	Sequence 73, Appli
15	1401	68.5	492	4	US-10-682-845-85	Sequence 85, Appli
16	1399	68.4	492	4	US-10-682-845-77	Sequence 77, Appli
17	1397	68.3	492	4	US-10-682-845-83	Sequence 75, Appli
18	1397	68.3	492	4	US-10-682-845-79	Sequence 83, Appli
19	1395	68.2	492	4	US-10-682-845-79	Sequence 79, Appli
20	1390	67.9	492	4	US-10-682-845-81	Sequence 81, Appli
21	1326.5	64.8	524	5	US-10-805-177-113	Sequence 113, Appli
22	1305	63.8	532	6	US-10-036-098-18	Sequence 18, Appli
23	1289	63.0	507	4	US-10-239-656-47	Sequence 47, Appli
24	1189.5	58.1	895	4	US-10-296-085A-19	Sequence 19, Appli
25	1189.5	58.1	895	4	US-10-296-085A-27	Sequence 27, Appli
26	1189.5	58.1	895	5	US-10-496-179-4	Sequence 4, Appli
27	1189.5	58.1	896	4	US-10-296-085A-17	Sequence 17, Appli

**ALIGNMENTS**

RESULT 1  
 US-10-743-697-1  
 ; Sequence 1, Application US/10743697  
 ; Publication No. US200501360501  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KUFER, PETER  
 ; APPLICANT: BERRY, MEERY  
 ; APPLICANT: BAEURLE, PATRICK  
 ; APPLICANT: ITIN, CHRISTIAN  
 ; TITLE OF INVENTION: BISPECIFIC ANTIBODIES  
 ; FILE REFERENCE: DEBE:028US  
 ; CURRENT APPLICATION NUMBER: US/10/743, 697  
 ; CURRENT FILING DATE: 2003-12-22  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 378  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: OTHER INFORMATION: Description of Artificial Sequence  
 ; OTHER INFORMATION: Peptide  
 ; OTHER INFORMATION: Description of Artificial Sequence  
 ; OTHER INFORMATION: Peptide  
 US-10-743-697-1

Query Match 100.0%; Score 2046; DB Best Local Similarity 100.0%; Pred. No. 9.9e-11  
 Matches 378; Conservative 0; Mismatches 0

QY 1 ELYNTQSPLSLTVTAGKVTNSCKSSQSLNSGNQKNN  
 Db 1 ELYNTQSPLSLTVTAGKVTNSCKSSQSLNSGNQKNN

QY 61 E5C9PDRFTGSGTDTLTTSSQARDLAVYQNN  
 Db 61 E5C9PDRFTGSGTDTLTTSSQARDLAVYQNN

QY 121 G5C9GGSB5VQLEQSGABLYVRPGTSKISKCSAGH  
 Db 121 G5C9GGSB5VQLEQSGABLYVRPGTSKISKCSAGH

QY 181 F5C9GNTIYNEKPGKQTIAKKSSTAYMQLSSLT  
 Db 181 F5C9GNTIYNEKPGKQTIAKKSSTAYMQLSSLT

QY 301 I5G9NPSRGYTNQKEKQKATLTDKSSSTAYMQLS  
 Db 301 I5G9NPSRGYTNQKEKQKATLTDKSSSTAYMQLS

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Sequence 2, Appli
Sequence 7, Appli
Sequence 28, Appli
Sequence 5, Appli
Sequence 20, Appli
Sequence 18, Appli
Sequence 3, Appli
Sequence 49, Appli
Sequence 48, Appli
Sequence 79, Appli
Sequence 75, Appli
Sequence 73, Appli
Sequence 77, Appli
Sequence 350, App
Sequence 115, App
Sequence 11, Appli
Sequence 221, App

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
; US-10-672-932-18

Query Match 72.6%; Score 1484.5; DB 5; Length 495;
Best Local Similarity 74.7%; Pred. No. 4.2e-91;
Matches 278; Conservative 34; Mismatches 53; Indels 7; Gaps 2;
Query 1 BLVMTQSPSLLTVAGBKVUTMSCKSSQSLINSLNGNQKNLTYWQKPGQPPKLUWASTR 60
Db 1 DIVLTQSPASISASAVGTVITCRASENIY----SILAWIQQOKQKSPLQVNLATL 54
Db 55 TRGVPSRSPSGSGTQFSIKLNSLOPEDPFGNYFCQHIDPRTFGGTBLKIGGGSGG 114
Query 121 GGGGGASBEVOLLEBOSAELVAPGTSKISCGASGAFTINYWLGMVKQRPQHGLWIGI 180
Db 115 GGGGGGSQVQ LQPGAGRVRPGASVTLKLSGAGSYFTSYMMWVQKQPGQGLEWIGI 173
Query 181 FPGSGNTHNEKPKGKATLTADKSSSTAYMQLSSLTEDSAVYCARLRLWDEPPMDYQ 240
Db 174 HPSDSETRLNQKENDRATLTVKYSTAYQLSPTSEDASAVYCARLRLWDEPPMDYQ 240
Query 241 GTTVTUVSSGGGSDIKLQSGARLPGASVMSCKSQTGTYTRTMHWYKQRPQGLEW 300
Db 234 GTTVTUVSSGGGSDIKLQSGARLPGASVMSCKSQTGTYTRTMHWYKQRPQGLEW 293
Query 301 IGYINPBRGTYINQKDKATLTDKSSSTAYMQLSSLTEDSAVYCARLRLWDEPPMDYQ 360
Db 294 IGYINPBRGTYINQKDKATLTDKSSSTAYMQLSSLTEDSAVYCARLRLWDEPPMDYQ 353
Query 361 YWQGQTTLVSS 372
Db 354 YWQGQTTLVSS 365

RESULT 4
US-10-168-809-22
; Sequence 22, Application US/10168809
; Publication No. US/0030180799A1
; GENERAL INFORMATION:
; APPLICANT: Müller-Hermelink, Hans Konrad
; APPLICANT: GREINER, AXEL
; APPLICANT: DORKEN, BEIND
; APPLICANT: BARGOU, RALF
; APPLICANT: KUFER, PETER
; TITLE OF INVENTION: ANTIBODIES AGAINST PLASMA CELLS
; FILE REFERENCE: 009848-0272/98
; CURRENT APPLICATION NUMBER: US/10/168,809
; CURRENT FILING DATE: 2002-06-21
; PRIORITY APPLICATION NUMBER: PCT/EP00/13338
; PRIORITY FILING DATE: 1999-12-23
; PRIORITY APPLICATION NUMBER: DE 199 62 593.2
; PRIORITY FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: 
; OTHER INFORMATION: Description of Artificial Sequence: synthetic hybrid, no
; OTHER INFORMATION: natural origin
Query Match 71.7%; Score 1467; DB 4; Length 500;
Best Local Similarity 76.4%; Pred. No. 6.2e-90;
Matches 285; Conservative 29; Mismatches 55; Indels 4; Gaps 4;
Query 301 IGYINPBRGTYINQKDKATLTDKSSSTAYMQLSSLTEDSAVYCARLRLWDEPPMDYQ 360
Db 294 IGYINPBRGTYINQKDKATLTDKSSSTAYMQLSSLTEDSAVYCARLRLWDEPPMDYQ 353
Query 361 YWQGQTTLVSS 372
Db 354 YWQGQTTLVSS 365

RESULT 3
US-10-672-932-18
; Sequence 18, Application US/10672932
; Publication No. US/003019170A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/10/672, 932
; CURRENT FILING DATE: 2003-09-26
; PRIORITY APPLICATION NUMBER: US/09/948, 004
; PRIORITY FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34

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Db 351 YWGGOTTIVSS 362

RESULT 7

; Sequence 61, Application US/10682845

; Publication No. US20040162411A1

; GENERAL INFORMATION:

; APPLICANT: Lanzavecchia, Antonio

; TITLE OF INVENTION: Potent T cell modulating molecules

; FILE REFERENCE: G2296 US

; CURRENT APPLICATION NUMBER: US/10/682,845

; CURRENT FILING DATE: 2003-10-10

; PRIOR APPLICATION NUMBER: US 60/419,149

; PRIOR FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: CA 2,403,313

; PRIOR FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 61

; LENGTH: 492

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE: OTHER INFORMATION: scFv EpcAMxCD3 with M76 mutant in anti-CD3 part

US-10-682-845-61

Query Match 68.9%; Score 1409; DB 4; Length 492; Best Local Similarity 71.0%; Pred. No. 4.6e-86; Mismatches 54; Indels 10; Gaps 4; Matches 264; Conservative 44; Mismatches 54; Indels 10; Gaps 4; Length: 492; Score: 1409; DB: 4; Best Local Similarity: 71.0%; Pred. No.: 4.6e-86; Mismatches: 54; Indels: 10; Gaps: 4; Matches: 264; Conservative: 44; Mismatches: 54; Indels: 10; Gaps: 4; SEQ ID NO 61

QY 1 ELVMTQSPSSLTVTAGEKUTMSCKSSQSLNSGNQKNVLTWYQOKPGOPPKLLIYMASTER 60

Db 1 DQ01050QKFMPSVQGDRVTSVCAQ-----NVGTNVAWQOKPGQSPKALIYASYR 54

QY 61 ESGYVDRFTGSGGMDFTLTISVQADIAVLAVYCCQNDSYPLTFAGTKEIKGGGSGG 120

Db 55 YSGVYDRAFTGSGGMDFTLTISVQADIAVLAVYCCQNDSYPLTFAGTKEIKGGGSGG 114

Qy 121 GSGGGGSEEVQLEQSGABELVPRGTSVYKISCIOSAGYAFNTYVILGWVWIKQRPQHGLEWQDI 180

Db 115 GSGGGGSSQVK-LQESQGLVQPSQSLSTCTVSGFSLISYGHVWIKQRPQHGLEWQDI 173

QY 181 FPGSGNIIHNBKFKKATLTADKSSTAYMQLSSLTEDSAVYFCARLNWDRPMQDYGQ 240

Db 174 WSG-GSTDNAAFTSRLSISKDNKSKQVFFKMSLQANDTAYCARMENNS--FAYWQ 230

QY 241 GTTVTVSSGGGSDIKLQOQGELARPGASVMSKCKTSGYTFRTYMHVKQRPQGLEW 300

Db 231 GTTVTVSSGGGSDIKLQOQGELARPGASVMSKCKTSGYTFRTYMHVKQRPQGLEW 290

QY 301 IGYINPSPGTYNTNQKFKKATLTADKSSTAYMQLSSLTEDSAVYFCARLYDDHQLD 360

Db 291 IGYINPSPGTYNTNQKFKKATLTADKSSTAYMQLSSLTEDSAVYFCARLYDDHQLD 350

QY 351 YWGGOTTIVSS 372

Db 351 YWGGOTTIVSS 362

RESULT 8

US-10-682-845-67

; Sequence 87, Application US/10682845

; Publication No. US20040162411A1

; GENERAL INFORMATION:

; APPLICANT: Lanzavecchia, Antonio

; TITLE OF INVENTION: Potent T cell modulating molecules

; FILE REFERENCE: G2296 US

; CURRENT APPLICATION NUMBER: US/10/682,845

; CURRENT FILING DATE: 2003-10-10

; PRIOR APPLICATION NUMBER: US 60/419,149

; PRIOR FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: CA 2,403,313

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 65

; LENGTH: 492

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE: OTHER INFORMATION: scFv EpcAMxCD3 with M76 mutant in anti-CD3 part

US-10-682-845-65

Query Match 68.7%; Score 1406; DB 4; Length 492; Best Local Similarity 71.0%; Pred. No. 7.2e-86; Mismatches 55; Indels 10; Gaps 4; Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4; Length: 492; Score: 1406; DB: 4; Best Local Similarity: 71.0%; Pred. No.: 7.2e-86; Mismatches: 55; Indels: 10; Gaps: 4; Matches: 264; Conservative: 43; Mismatches: 55; Indels: 10; Gaps: 4; SEQ ID NO 65

QY 1 ELVMTQSPSSLTVTAGEKUTMSCKSSQSLNSGNQKNVLTWYQOKPGOPPKLLIYMASTER 60

RESULT 10  
 US-10-682-845-67  
 ; Sequence 67, Application US/10682845  
 ; Publication No. US20040162411A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lanzavecchia, Antonio  
 ; TITLE OF INVENTION: Potent T cell modulating molecules  
 ; FILE REFERENCE: G2296 US  
 ; CURRENT APPLICATION NUMBER: US/10/682,845  
 ; CURRENT FILING DATE: 2003-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/419,149  
 ; PRIOR FILING DATE: 2002-10-18  
 ; PRIOR APPLICATION NUMBER: CA 2,403,313  
 ; PRIOR FILING DATE: 2002-10-11  
 ; NUMBER OF SEQ ID NOS: 89  
 ; SEQ ID NOS: 1-89  
 ; SOFTWARE: Patentin version 3.1  
 ; LENGTH: 492  
 ; TYPE: PRT  
 ; ORGANISM: artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: scFv EpcamxCD3 with M4 mutant in anti-CD3 part  
 ; US-10-682-845-67  
 Query Match Similarity 68.7%; Score 1405; DB 4; Length 492;  
 Best Local Similarity 71.0%; Pred. No. 8.4e-86; Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;  
 Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;  
 Query 1 BLUMTQSPSSLTIVTACKVMSCKSSQSLNSGNQKNYLWYQKRGQPPKLUITWASTR 60  
 Db 1 DIOLOTQSKFMTSIVGDRVSVTICKASQ----NGTNVAVWQOQKPGQSPKALISASR 54  
 Db 61 ESGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 120  
 Query 55 YSGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 114  
 Db 121 GSGGGGSEVQLEQSGAELVRPGTSVKSCKASGYAFTNYWLGWVQRPQHGLEWGD 180  
 Query 61 ESGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 120  
 Db 55 YSGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 114  
 Query 121 GSGGGGSEVQLEQSGAELVRPGTSVKSCKASGYAFTNYWLGWVQRPQHGLEWGD 180  
 Db 115 GSGGGGSGQVK-LQESGGPLVQPSQSLSLTCTVSGFSUTSYGHMWRQSPGKLEWGV 173  
 Query 181 FPGSGNTHYNEKFRGKATLTDKKSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 240  
 Db 174 WSG-GSTDYNAFAFISRLSISKDKNSKQVFFKMSLQANDTAYCARMENWS-FAWWQ 230  
 Query 241 GTTVTVSSGGGSDIKUQSGAELARPGASVMSCKTSQGFTTRYTMHWKORPGQGLEW 300  
 ; RESULT 12  
 ; Sequence 71, Application US/10682845  
 ; Publication No. US20040162411A1  
 Query 301 IGYINPRSGYTYNQKFKDQKATLTDKSSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 290  
 Db 291 IGYINPRSGYTYNQKFKDQKATLTDKSSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 350  
 Db 351 YWGQTTLTWSS 372  
 Query 351 YWGQTTLTWSS 362  
 ; RESULT 11  
 US-10-682-845-63  
 ; Sequence 63, Application US/10682845  
 ; Publication No. US20040162411A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lanzavecchia, Antonio  
 ; TITLE OF INVENTION: Potent T cell modulating molecules  
 ; FILE REFERENCE: G2296 US  
 ; CURRENT APPLICATION NUMBER: US/10/682,845  
 ; CURRENT FILING DATE: 2003-10-10  
 ; PRIOR APPLICATION NUMBER: CA 2,403,313  
 ; PRIOR FILING DATE: 2002-10-11  
 ; PRIOR APPLICATION NUMBER: CA 2,403,313  
 ; PRIOR FILING DATE: 2002-10-11  
 ; NUMBER OF SEQ ID NOS: 89  
 ; SEQ ID NO: 63  
 ; LENGTH: 492  
 ; TYPE: PRT  
 ; ORGANISM: artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: scFv EpcamxCD3 with M4 mutant in anti-CD3 part  
 ; US-10-682-845-63  
 Query Match Similarity 68.7%; Score 1405; DB 4; Length 492;  
 Best Local Similarity 71.0%; Pred. No. 8.4e-86; Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;  
 Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;  
 Query 1 BLUMTQSPSSLTIVTACKVMSCKSSQSLNSGNQKNYLWYQKRGQPPKLUITWASTR 60  
 Db 1 DIOLOTQSKFMTSIVGDRVSVTICKASQ----NGTNVAVWQOQKPGQSPKALISASR 54  
 Db 61 ESGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 120  
 Query 55 YSGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 114  
 Db 121 GSGGGGSEVQLEQSGAELVRPGTSVKSCKASGYAFTNYWLGWVQRPQHGLEWGD 180  
 Query 61 ESGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 120  
 Db 55 YSGVPRPRTGGSGIDFTLTISSVQAEPLAVYCYONDYSPLTFGAGTKLKEKGGS 114  
 Query 121 GSGGGGSEVQLEQSGAELVRPGTSVKSCKASGYAFTNYWLGWVQRPQHGLEWGD 180  
 Db 115 GSGGGGSGQVK-LQESGGPLVQPSQSLSLTCTVSGFSUTSYGHMWRQSPGKLEWGV 173  
 Query 181 FPGSGNTHYNEKFRGKATLTDKKSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 240  
 Db 174 WSG-GSTDYNAFAFISRLSISKDKNSKQVFFKMSLQANDTAYCARMENWS-FAWWQ 230  
 Query 241 GTTVTVSSGGGSDIKUQSGAELARPGASVMSCKTSQGFTTRYTMHWKORPGQGLEW 300  
 ; RESULT 12  
 ; Sequence 71, Application US/10682845  
 ; Publication No. US20040162411A1  
 Query 301 IGYINPRSGYTYNQKFKDQKATLTDKSSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 290  
 Db 291 IGYINPRSGYTYNQKFKDQKATLTDKSSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 350  
 Db 351 YWGQTTLTWSS 372  
 ; RESULT 12  
 ; Sequence 71, Application US/10682845  
 ; Publication No. US20040162411A1  
 Query 301 IGYINPRSGYTYNQKFKDQKATLTDKSSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 290  
 Db 291 IGYINPRSGYTYNQKFKDQKATLTDKSSSTAYMQLSLTFTEDSAVFCARLNWDPEMDWQ 350  
 Db 351 YWGQTTLTWSS 362

; GENERAL INFORMATION:  
; APPLICANT: LanzaVecchia, Antonio  
; FILE REFERENCE: Potent T cell modulating molecules  
; CURRENT APPLICATION NUMBER: US/10/682,845  
; PRIOR APPLICATION NUMBER: US 60/419,149  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: CA 2,403,313  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 71  
; LENGTH: 492  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE: OTHER INFORMATION: scFv EpcamxCD3 with M10 mutant in anti-CD3 part  
; US-10-682-845-71  
; Query Match 68.6%; Score 1404; DB 4; Length 492;  
; Best Local Similarity 71.0%; Pred. No. 9; Be-86;  
; Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;  
; Qy 1 ELVMTQSSSLTVAGEKUTMSCKSSQSLNSGQKNTLTWQKPGQPPKKLIYMASTR 60  
; Db 1 DIQITQSQKFMSTSVGRDVSITKASQ----NVGTVNVAWQOKPGQSPKALIYSYR 54  
; Db 1 DIQITQSQKFMSTSVGRDVSITKASQ----NVGTVNVAWQOKPGQSPKALIYSYR 54  
; Qy 61 ESGVDPRTGSGSGTDFLTISVQAEIDLAVYCCNDYSYPLTFGAGTKLEIKGGGG 120  
; Db 61 ESGVDPRTGSGSGTDFLTISVQAEIDLAVYCCNDYSYPLTFGAGTKLEIKGGGG 120  
; Db 55 YSGVDPRTGSGSGTDFLTISVQAEIDLAVYCCNDYSYPLTFGAGTKLEIKGGGG 114  
; Db 121 GGGGGGSEVOLQLEQSGAELVRPGTSVKISCKASGYAFTNYLQGKVKORPGHGLEWID 180  
; Qy 121 GGGGGGSEVOLQLEQSGAELVRPGTSVKISCKASGYAFTNYLQGKVKORPGHGLEWID 180  
; Db 115 GGGGGGSGQVK-LQESGGGLVQPSQSLSLTCTVSGRSITSYGHVWQSPKGLEWIGV 173  
; Qy 181 FPGSGNITHNEKEPKKATLTADKSSTAMQLOSSLTPEDSAUVFCARLNRNWPMDYNGQ 240  
; Db 174 WSG-GSTDYNAFAFISRLSISKDNRSQVFPKMSLQANDTAYCARMENWS--FAYWGQ 230  
; Qy 241 GTTVTVVSSGGGSDIKLQOQSGAELARPGASVMSCKTSGYTFRTYTMHWKQRPQGLEW 300  
; Db 231 GTTVTVVSSGGGSDIKLQOQSGAELARPGASVMSCKTSGYTFRTYTMHWKQRPQGLEW 290  
; Qy 301 IGYINPSRGYTNQKFKATLTDDKSSTAYMQLSSLTSDAVYCARVYDDHYCLD 360  
; Db 291 IGYINPSRGYTNQKFKATLTDDKSSTAYMQLSSLTSDAVYCARVYDDHYCLD 350  
; Qy 361 YWGGOTTITVSS 372  
; Db 351 YWGGOTTITVSS 362  
; RESULT 13  
; US-10-682-845-69  
; Sequence 69, Application US/10682845  
; Publication No. US2004016241A1  
; GENERAL INFORMATION:  
; APPLICANT: LanzaVecchia, Antonio  
; FILE REFERENCE: Potent T cell modulating molecules  
; CURRENT APPLICATION NUMBER: US/10/682,845  
; PRIOR APPLICATION NUMBER: US 60/419,149  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: CA 2,403,313  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 73  
; LENGTH: 492  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE: OTHER INFORMATION: scFv EpcamxCD3 with M13 mutant in anti-CD3 part  
; US-10-682-845-73  
; Query Match 68.5%; Score 1401; DB 4; Length 492;  
; Best Local Similarity 70.7%; Pred. No. 1; Be-85;  
; Matches 263; Conservative 44; Mismatches 55; Indels 10; Gaps 4;  
; Qy 1 ELVMTQSSSLTVAGEKUTMSCKSSQSLNSGQKNTLTWQKPGQPPKKLIYMASTR 60  
; Db 1 DIQITQSQKFMSTSVGRDVSITKASQ----NVGTVNVAWQOKPGQSPKALIYSYR 54  
; Qy 61 ESGVDPRTGSGSGTDFLTISVQAEIDLAVYCCNDYSYPLTFGAGTKLEIKGGGG 120  
; Db 55 YSGVDPRTGSGSGTDFLTISVQAEIDLAVYCCNDYSYPLTFGAGTKLEIKGGGG 114



116 Page Blank (uspto)



CC of one antibody variable domain; and a second portion of the bispecific antibody is capable of specifically binding to a target antigen other than the effector antigen, the target antigen being located on a target cell other than the human immune effector cell, and the second portion comprising an antibody variable domain. The bispecific antibody is useful in preparing a composition for treating, preventing or ameliorating a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, a viral disease, an allergic reaction, a parasitic reaction, a graft-versus-host disease or a host-versus-graft disease. This sequence corresponds to the chimeric anti-CD3xanti-EpCAM bispecific antibody of the invention.

XX SQ Sequence 378 AA;

Query Match 100.0%; Score 2046; DB 9; Length 378;  
Best Local Similarity 100.0%; Pred. No. 1.1e-119; Mismatches 0; Indels 0; Gaps 0;  
Matches 378; Conservative 0; N mismatches 0; Del 0; Insert 0;

Qy 1 ELYMTOSSSLTIVTAGEKYTMCKSQSOLNSNQKNTLYWQOKPGQPPKLLYMASTER 60  
1 ELYMTOSSSLTIVTAGEKYTMCKSQSOLNSNQKNTLYWQOKPGQPPKLLYMASTER 60

Qy 61 ESGYDPDRFGSGGDFLTISQVQAEIDLAVYKQNDISYPLTFAGAKTLEIKGGGGGG 120  
61 ESGYDPDRFGSGGDFLTISQVQAEIDLAVYKQNDISYPLTFAGAKTLEIKGGGGGG 120

Db 121 GGSQQGGSSEVOLLBQSGAELVRPGSVKISKASGQAFPTNYWLGWVKORPGHLEWIDI 180  
121 GGSQQGGSSEVOLLBQSGAELVRPGSVKISKASGQAFPTNYWLGWVKORPGHLEWIDI 180

Qy 181 FPGSGNITHNEPKKGATLTADKSSTAMQQLSSLTEDSAVFCARLNWDRPMYQGQ 240  
181 FPGSGNITHNEPKKGATLTADKSSTAMQQLSSLTEDSAVFCARLNWDRPMYQGQ 240

Db 241 GTTVTVSSGGGSDIKLQOQSGAELARPGASVRSVMSCKTSGYTFRTYMHVKORPGQGLEW 300  
241 GTTVTVSSGGGSDIKLQOQSGAELARPGASVRSVMSCKTSGYTFRTYMHVKORPGQGLEW 300

Qy 301 IGYINPSRGYNTNQKFQDKATLTIDKSSTAYMQLSSLTEDSAVYCARYYDDHYCLD 360  
301 IGYINPSRGYNTNQKFQDKATLTIDKSSTAYMQLSSLTEDSAVYCARYYDDHYCLD 360

Db 361 YWGOQTTLTVSSHHHHH 378  
361 YWGOQTTLTVSSHHHHH 378

RESULT 2  
ADV6121  
ID ADV6121 standard; protein; 521 AA.  
AC ADV6121;  
XX DT 24-FEB-2005 (first entry)  
XX DB Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 44.  
XX KW bispecific single chain antibody; epithelial cell adhesion molecule;  
KW EpCAM; CD3; tumor; cancer; cytostatic.  
XX OS Unidentified.  
XX WO2004106383-A1.  
XX PD 09-DEC-2004.  
XX PF 26-MAY-2004; 2004WO-EP005687.  
XX PR 31-MAY-2003; 2003EP-00012133.  
PR 31-MAY-2003; 2003EP-00012134.  
XX PA (MICR-) MICROMET AG.  
XX

PI Kufner P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;  
PT Kohleien B, Lenkner-Schuetz U, Bauerle P;  
XX DR WPI; 2005-031271/02.  
N-PSDB; ADV6120.

PT New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.  
XX PS Claim 12; SEQ ID NO 44; 227pp; English.

XX SQ Sequence 521 AA;

Query Match 97.7%; Score 1998; DB 9; Length 521;  
Best Local Similarity 100.0%; Pred. No. 1.5e-116; Mismatches 0; Indels 0; Gaps 0;  
Matches 372; Conservative 0; N mismatches 0; Del 0; Insert 0;

Qy 1 ELYMTOSSSLTIVTAGEKYTMCKSQSOLNSNQKNTLYWQOKPGQPPKLLYMASTER 60  
1 ELYMTOSSSLTIVTAGEKYTMCKSQSOLNSNQKNTLYWQOKPGQPPKLLYMASTER 60

Db 20 ELYMTOSSSLTIVTAGEKYTMCKSQSOLNSNQKNTLYWQOKPGQPPKLLYMASTER 79

Qy 61 ESGYDPDRFGSGGDFLTISQVQAEIDLAVYKQNDISYPLTFAGAKTLEIKGGGGGG 120  
61 ESGYDPDRFGSGGDFLTISQVQAEIDLAVYKQNDISYPLTFAGAKTLEIKGGGGGG 120

Db 80 ESGYDPDRFGSGGDFLTISQVQAEIDLAVYKQNDISYPLTFAGAKTLEIKGGGGGG 139

Qy 121 GGSQQGGSSEVOLLBQSGAELVRPGSVKISKASGQAFPTNYWLGWVKORPGHLEWIDI 180  
121 GGSQQGGSSEVOLLBQSGAELVRPGSVKISKASGQAFPTNYWLGWVKORPGHLEWIDI 180

Db 140 GGSQQGGSSEVOLLBQSGAELVRPGSVKISKASGQAFPTNYWLGWVKORPGHLEWIDI 199  
140 GGSQQGGSSEVOLLBQSGAELVRPGSVKISKASGQAFPTNYWLGWVKORPGHLEWIDI 199

Qy 181 FPGSGNITHNEPKKGATLTADKSSTAMQQLSSLTEDSAVFCARLNWDRPMYQGQ 240  
181 FPGSGNITHNEPKKGATLTADKSSTAMQQLSSLTEDSAVFCARLNWDRPMYQGQ 240

Db 200 FPGSGNITHNEPKKGATLTADKSSTAMQQLSSLTEDSAVFCARLNWDRPMYQGQ 259  
200 FPGSGNITHNEPKKGATLTADKSSTAMQQLSSLTEDSAVFCARLNWDRPMYQGQ 259

Qy 241 GTTVTVSSGGGSDIKLQOQSGAELARPGASVRSVMSCKTSGYTFRTYMHVKORPGQGLEW 300  
241 GTTVTVSSGGGSDIKLQOQSGAELARPGASVRSVMSCKTSGYTFRTYMHVKORPGQGLEW 300

Db 320 GTTVTVSSGGGSDIKLQOQSGAELARPGASVRSVMSCKTSGYTFRTYMHVKORPGQGLEW 319  
320 GTTVTVSSGGGSDIKLQOQSGAELARPGASVRSVMSCKTSGYTFRTYMHVKORPGQGLEW 319

Qy 361 YWGOQTTLTVSS 372  
361 YWGOQTTLTVSS 372

Db 380 YWGOQTTLTVSS 391  
380 YWGOQTTLTVSS 391

RESULT 3  
ADV6116  
ID ADV6116 standard; protein; 521 AA.  
AC ADV6116;  
XX DT 24-FEB-2005 (first entry)  
XX DB Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 39.  
XX KW bispecific single chain antibody; epithelial cell adhesion molecule;  
KW EpCAM; CD3; tumor; cancer; cytostatic.  
XX OS Unidentified.  
XX WO2004106383-A1.

PD 09-DEC-2004.  
 XX  
 PF 26-MAY-2004; 2004WO-EP005687.  
 XX  
 PR 31-MAY-2003; 2003EP-00012133.  
 XX  
 PR 31-MAY-2003; 2003EP-00012134.  
 XX  
 PA (MICR-) MICROMET AG.  
 XX  
 PI Kuper P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;  
 PI Kohleisen B, Lenkkeri-Schuetz U, Bauerle P;  
 XX  
 DR N-PSDB; ADN6615.  
 XX  
 PT New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.  
 XX  
 PT Claim 12; SEQ ID NO 39; 227pp; English.  
 CC The invention comprises a composition that contains a bispecific single chain antibody consisting of at least two domains, where one of domains binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the second domain binds to human CD3 antigen. The bispecific antibody construct of the invention is useful for the prevention, treatment or amelioration of a tumorous disease, such as an epithelial or minimal residual cancer. The present amino acid sequence represents a bispecific single chain antibody of the invention.  
 XX  
 SQ Sequence 521 AA;  
 Query Match 94.6%; Score 1935; DB 9; Length 521;  
 Best Local Similarity 97.0%; Pred. No. 1.2e-112; Mismatches 361; Conservative 3; Indels 0; Gaps 0;  
 Matches 361; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 60  
 Db 20 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 79  
 Qy 61 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 120  
 Db 80 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 139  
 Qy 121 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 180  
 Db 140 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 199  
 XX  
 SQ Sequence 496 AA;  
 Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best Local Similarity 95.2%; Pred. No. 2.4e-112; Mismatches 354; Conservative 12; Mismatches 354; Conservative 12; Mismatches 0;  
 Matches 354; Conservative 12; Mismatches 0;  
 Qy 1 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 60  
 Db 1 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 60  
 Qy 61 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 120  
 Db 61 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 120  
 Qy 121 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 180  
 Db 121 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 180  
 XX  
 RESULT 4  
 AD28353 AD28353 standard; protein; 496 AA.  
 XX  
 AC AD283653; 14-JUL-2005 (first entry)

DE CD3 specific binding construct SEQ ID NO 275.  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antiflammatory;  
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic;  
 KW Synthetic.  
 OS  
 XX  
 PN WO2005040220-A1.  
 XX  
 PD 06-MAY-2005.  
 XX  
 WO2005040220-A1.  
 XX  
 15-OCT-2004; 2004WO-EP011646.  
 XX  
 PR 16-OCT-2003; 2003EP-00023581.  
 XX  
 DR N-PSDB; AD283652.  
 XX  
 PT Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Bauerle P;  
 PI Carr FJ, Hamilton AA, Williams S;  
 XX  
 DR WPI; 2005-333494/34.  
 XX  
 New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second domain, useful for treating, preventing, or ameliorating, e.g. PT proliferative disease.  
 XX  
 SQ Claim 20; SEQ ID NO 275; 639pp; English.  
 XX  
 The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The cytotoxically active CD3 specific binding construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft disease. The present sequence represents the amino acid sequence of a CD3 specific binding construct.  
 XX  
 SQ Sequence 496 AA;  
 Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best Local Similarity 95.2%; Pred. No. 2.4e-112; Mismatches 354; Conservative 12; Mismatches 354; Conservative 12; Mismatches 0;  
 Matches 354; Conservative 12; Mismatches 0;  
 Qy 1 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 60  
 Db 1 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 60  
 Qy 61 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 120  
 Db 61 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 120  
 Qy 121 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 180  
 Db 121 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 180  
 XX  
 Qy 181 FPGSGNHYNEKFKGKLTADKSSSTAYMQLSSLTFFEDSVFCARLRAWDEPMWQ 240  
 Db 200 FPGSGNHYNEKFKGKLTADKSSSTAYMQLSSLTFFEDSVFCARLRAWDEPMWQ 259  
 Qy 241 GTIVTVSSGGGSDIKLQSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 300  
 Db 260 GTIVTVSSGGGSDIKLQSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 319  
 Qy 301 IGYINPSPRGYTYNQKFDKLTITDKSSSTAYMQLSSLTFFEDSVFCARLYDDYCLD 360  
 Db 320 IGYINPSPRGYTYNQKFDKLTITDKSSSTAYMQLSSLTFFEDSVFCARLYDDYCLD 379  
 Qy 361 YNGQGTTLTIVSS 372  
 Db 380 YNGQGTTLTIVSS 391  
 XX  
 RESULT 4  
 AD28353 AD28353 standard; protein; 496 AA.  
 XX  
 AC AD283653; 14-JUL-2005 (first entry)

DE CD3 specific binding construct SEQ ID NO 275.  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antiflammatory;  
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic;  
 KW Synthetic.  
 OS  
 XX  
 PN WO2005040220-A1.  
 XX  
 PD 06-MAY-2005.  
 XX  
 WO2005040220-A1.  
 XX  
 15-OCT-2004; 2004WO-EP011646.  
 XX  
 PR 16-OCT-2003; 2003EP-00023581.  
 XX  
 DR N-PSDB; AD283652.  
 XX  
 PT Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Bauerle P;  
 PI Carr FJ, Hamilton AA, Williams S;  
 XX  
 DR WPI; 2005-333494/34.  
 XX  
 New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second domain, useful for treating, preventing, or ameliorating, e.g. PT proliferative disease.  
 XX  
 SQ Claim 20; SEQ ID NO 275; 639pp; English.  
 XX  
 The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The cytotoxically active CD3 specific binding construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft disease. The present sequence represents the amino acid sequence of a CD3 specific binding construct.  
 XX  
 SQ Sequence 496 AA;  
 Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best Local Similarity 95.2%; Pred. No. 2.4e-112; Mismatches 354; Conservative 12; Mismatches 354; Conservative 12; Mismatches 0;  
 Matches 354; Conservative 12; Mismatches 0;  
 Qy 1 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 60  
 Db 1 ELVMTQSPSSITVTAGEKVINSCKSSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 60  
 Qy 61 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 120  
 Db 61 ESGVPDRFTGSGSGDFLTISVQADLAVYQNDYSPLTIFGAGTKLEIKGGGG 120  
 Qy 121 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 180  
 Db 121 GSGGGGSEVOLLEQSGAELVRPGTISKASGGAFTNWLGVWKRQPGHLEWIGDI 180  
 XX  
 Qy 181 FPGSGNHYNEKFKGKLTADKSSSTAYMQLSSLTFFEDSVFCARLRAWDEPMWQ 240  
 Db 181 FPGSGNHYNEKFKGKLTADKSSSTAYMQLSSLTFFEDSVFCARLRAWDEPMWQ 240  
 Qy 241 GTIVTVSSGGGSDIKLQSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 300  
 Db 241 GTIVTVSSGGGSDIKLQSQSLNSGNGQKLYTWQKPGQPPKLUITWASTR 300

QY 301 IGYINPSQTYNTNQKFKAQKATLTDKSSTAYMQLSSLTEDSAVYCARYDDYCLD 360  
 DB 301 IGYINPSQTYNTNQKFKAQKATLTDKSSTAYMQLSSLTEDSAVYCARYDDYCLD 360  
 QY 361 YWQGQTTIVVSS 372  
 DB AD283637  
 RESULT 5  
 ID AD283637 standard; protein; 496 AA.  
 XX  
 AC AD283637;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 CD3 specific binding construct SEQ ID NO 259.  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytotoxic; Antinflammatory;  
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005040220-A1.  
 PD 06-MAY-2005.  
 XX  
 PP 15-OCT-2004; 2004WO-EP011646.  
 XX  
 PR 16-OCT-2003; 2003EP-00023581.  
 PA (MCR-) MICROMET AG.  
 XX  
 PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baauerle P;  
 PI Carr FJ, Hamilton AA, Williams S;  
 XX  
 DR WPI; 2005-333494/34.  
 DR N-ISDB; AD283636.  
 XX  
 PT New cytotoxicity active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.  
 XX  
 PS Claim 20, SEQ ID NO 259; 639pp; English.  
 XX  
 The invention relates to a cytotoxicity active CD3 specific binding  
 construct comprises a first domain specifically binding to human CD3 and  
 an Ig-derived second binding domain. The CD3 specific binding construct  
 above or the construct produced by the process, nucleic acid molecule,  
 vector, or host is useful for the preparation of a pharmaceutical  
 composition for the prevention, treatment, or amelioration of a  
 proliferative disease, a tumor, an inflammatory disease, an immunological  
 disorder, an autoimmune disease, an infectious disease, viral disease,  
 allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 host-versus-graft diseases. The cytotoxicity active CD3 specific binding  
 construct is useful for treating, preventing, or ameliorating  
 proliferative disease, a tumor, an inflammatory disease, an immunological  
 disorder, an autoimmune disease, an infectious disease, viral disease,  
 allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 host-versus-graft diseases. The present sequence represents the amino  
 acid sequence of a CD3 specific binding construct.  
 XX  
 Sequence 496 AA;

SQ Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best local Similarity 95.2%; Pred. No. 2.4e-112;  
 Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

DB 1 ELVMTQSSSLTVAGKVTMCKSSQSLISNGNQKLYLTWYQQPGQQPKLLIYMASTR 60  
 QY 61 ESCVPDFRTGSQSGTDTLTSSVQADLAVYCYDQSYPLTFGACTKLEIKGGGG 120  
 DB 61 ESCVPDFRTGSQSGTDTLTSSVQADLAVYCYDQSYPLTFGACTKLEIKGGGG 120  
 QY 121 GGGGGGSEVOLQSGELVRGTSVMSKSCASGTYFTWQKQRPHGLEWIGDI 180  
 DB 121 GGGGGGSEVOLQSGELVRGTSVMSKSCASGTYFTWQKQRPHGLEWIGDI 180  
 QY 181 FPGSGNINHYNEKEFKQKAQKATLTDKSSTAYMQLSSLTEDSAVYCARYDDYCLD 240  
 DB 181 FPGSGNINHYNEKEFKQKAQKATLTDKSSTAYMQLSSLTEDSAVYCARYDDYCLD 240  
 QY 241 GTTVTVSSGGGSDVOLQSGAVKKGAVSKVSKRASGYFTTYWVWVROAPGQLEW 300  
 DB 241 GTTVTVSSGGGSDVOLQSGAVKKGAVSKVSKRASGYFTTYWVWVROAPGQLEW 300  
 QY 301 IGYINPSQTYNTNQKFKAQKATLTDKSSTAYMQLSSLTEDSAVYCARYDDYCLD 360  
 DB 301 IGYINPSQTYNTNQKFKAQKATLTDKSSTAYMQLSSLTEDSAVYCARYDDYCLD 360  
 QY 361 YWQGQTTIVVSS 372  
 DB 361 YWQGQTTIVVSS 372

RESULT 6  
 ID AD283645  
 ID AD283645 standard; protein; 496 AA.  
 XX  
 AC AD283645;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 CD3 specific binding construct SEQ ID NO 267.  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytotoxic; Antinflammatory;  
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005040220-A1.  
 PD 06-MAY-2005.  
 XX  
 PP 15-OCT-2004; 2004WO-EP011646.  
 XX  
 PR 16-OCT-2003; 2003EP-00023581.  
 PA (MCR-) MICROMET AG.  
 XX  
 PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baauerle P;  
 PI Carr FJ, Hamilton AA, Williams S;  
 XX  
 DR WPI; 2005-333494/34.  
 DR N-ISDB; AD283644.  
 XX  
 PT New cytotoxicity active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.  
 XX  
 PS Claim 20, SEQ ID NO 267; 639pp; English.  
 XX  
 The invention relates to a cytotoxicity active CD3 specific binding  
 construct comprises a first domain specifically binding to human CD3 and  
 an Ig-derived second binding domain. The CD3 specific binding construct  
 above or the construct produced by the process, nucleic acid molecule,  
 vector, or host is useful for the preparation of a pharmaceutical  
 composition for the prevention, treatment, or amelioration of a

CC proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The cytotoxicically active CD3 specific binding construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 94.3%; Score 1930; DB 9; Length 496;

Best Local Similarity 95.2%; Pred. No. 2.4e-112; Mismatches 354; Conservative 12; Indels 0; Gaps 0;

Matches 354; No. 2.4e-112; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELMWQSPLITVAGEKVUMCKSSQSLSNLSGKRNLYTWYQKPGQPKLILWASTR 60

1 ELMWQSPLITVAGEKVUMCKSSQSLSNLSGKRNLYTWYQKPGQPKLILWASTR 60

Db 61 ESGVDPRTFGSGSGDFTLITISSQAEQDIAVYVCONDXSYPLTFCAGTLEIKGGSGC 120

61 ESGVDPRTFGSGSGDFTLITISSQAEQDIAVYVCONDXSYPLTFCAGTLEIKGGSGC 120

Db 121 GGSGGGSEVOLLESGAELVRPGTSVKSCKASGYAFTNYWLGWVKQRGHGLEWIDI 180

121 GGSGGGSEVOLLESGAELVRPGTSVKSCKASGYAFTNYWLGWVKQRGHGLEWIDI 180

Db 181 FPGSENTHYNEKFKEKATLTDKSSSTAYMQLSSLTPEFSAVYCARLRWDEPMWQ 240

181 FPGSENTHYNEKFKEKATLTDKSSSTAYMQLSSLTPEFSAVYCARLRWDEPMWQ 240

Db 241 GTTVTVSSGGSGSDIKLQSGAELARPAGSVMSCKTSGYTFTRTMHWVQPGQCGLEW 300

241 GTTVTVSSGGSGSDIKLQSGAELARPAGSVMSCKTSGYTFTRTMHWVQPGQCGLEW 300

QY 301 IGYINPSRGYTYNOKFKDQATLTDKSSSTAYMQLSSLTSEDSAVYCARYYDDHYCL 360

301 IGYINPSRGYTYNOKFKDQATLTDKSSSTAYMQLSSLTSEDSAVYCARYYDDHYCL 360

Db 361 YWGQGTITVTVSS 372

361 YWGQGTITVTVSS 372

Db

RESULT 7

ADZB3615

ID ADZB3615 Standard; protein; 496 AA.

XX

AC ADZB3615;

XX

DT 14-JUL-2005 (first entry)

XX

DE CD3 specific binding construct SEQ ID NO 237.

XX

KW neoplasm; inflammation; immune disorder; infection; allergy;

KW graft versus host disease; Cytostatic; Antiinflammatory;

KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.

OS Synthetic.

XX

PN WO2005040220-A1.

PD 06-MAY-2005.

XX

PP 15-OCT-2004; 2004WO-EP011646.

XX

PR 16-OCT-2003; 2003EP-00023581.

XX

PA (MICR-) MICROMET AG.

XX

PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Bauerle P;

XX Sequence 496 AA;

Query Match 92.5%; Score 1892; DB 9; Length 496;

Best Local Similarity 93.5%; Pred. No. 5.6e-110; Mismatches 12; Indels 0; Gaps 0;

Matches 348; No. 5.6e-110; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELMWQSPLITVAGEKVUMCKSSQSLSNLSGKRNLYTWYQKPGQPKLILWASTR 60

1 ELMWQSPLITVAGEKVUMCKSSQSLSNLSGKRNLYTWYQKPGQPKLILWASTR 60

Db 61 ESGVDPRTFGSGSGDFTLITISSQAEQDIAVYVCONDXSYPLTFCAGTLEIKGGSGC 120

61 ESGVDPRTFGSGSGDFTLITISSQAEQDIAVYVCONDXSYPLTFCAGTLEIKGGSGC 120

Db 121 GGSGGGSEVOLLESGAELVRPGTSVKSCKASGYAFTNYWLGWVKQRGHGLEWIDI 180

121 GGSGGGSEVOLLESGAELVRPGTSVKSCKASGYAFTNYWLGWVKQRGHGLEWIDI 180

Db 181 FPGSENTHYNEKFKEKATLTDKSSSTAYMQLSSLTPEFSAVYCARLRWDEPMWQ 240

181 FPGSENTHYNEKFKEKATLTDKSSSTAYMQLSSLTPEFSAVYCARLRWDEPMWQ 240

Db 241 GTTVTVSSGGSGSDIKLQSGAELARPAGSVMSCKTSGYTFTRTMHWVQPGQCGLEW 300

241 GTTVTVSSGGSGSDIKLQSGAELARPAGSVMSCKTSGYTFTRTMHWVQPGQCGLEW 300

QY 301 IGYINPSRGYTYNOKFKDQATLTDKSSSTAYMQLSSLTSEDSAVYCARYYDDHYCL 360

301 IGYINPSRGYTYNOKFKDQATLTDKSSSTAYMQLSSLTSEDSAVYCARYYDDHYCL 360

Db 361 YWGQGTITVTVSS 372

361 YWGQGTITVTVSS 372

Db

RESULT 8

ADZB3629

ID ADZB3629 Standard; protein; 496 AA.

XX

AC ADZB3629;

XX

DT 14-JUL-2005 (first entry)

XX

DE CD3 specific binding construct SEQ ID NO 251.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

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PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

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domain specifically binding to human CD3 and an Ig-derived second binding

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PT proliferative disease.

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PI Carr FU, Hamilton AA, Williams S;

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DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

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domain, useful for treating, preventing, or ameliorating, e.g.

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PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

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domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

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PI Carr FU, Hamilton AA, Williams S;

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DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

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PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

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PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

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PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

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PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

PT proliferative disease.

XX

PI Carr FU, Hamilton AA, Williams S;

XX

DR WPI; 2005-333494/34.

XX N-PSDB; ADZB3614.

XX&lt;/div

XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytotoxic; Antiinflammatory;  
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic;  
 KW Synthetic.

OS WO2005040220-A1.

PN XX

PD XX

06-MAY-2005.

XX

PR XX

15-OCT-2004; 2004WO-EP011646.

XX

PA (MICR-) MICROMET AG.

XX

PI Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Bauerle P;  
 Carr FU, Hamilton AA, Williams S;

XX DR WPI; 2005-333494/34.

XX DR N-FSDB; ADZ83628.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g. proliferative disease.

PS Claim 20; SEQ ID NO 251; 639pp; English.

XX

CC The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, or allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft diseases. The cytotoxically active CD3 specific binding construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, or allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.

XX

SQ Sequence 496 AA;

Query Match 92.5%; Score 1892; DB 9; Length 496;  
 Best Local Similarity 93.5%; Pred. No. 5.6e-110; Indels 0; Gaps 0;  
 Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY

1 BLVMTQSPSLLTIVAGKVTMSCKSSQSLNSQNLNSQNLWYQKPGQPPKLLIYASIR 60

Db 1 BLVWQSPSLLTIVAGKVTMSCKSSQSLNSQNLNSQNLWYQKPGQPPKLLIYASIR 60

QY 61 ESGVDRFTGSGMDPTLTISSVQAEADLWVYCONDYKPLTGGAGTKLEIKGGGGCG 120

Db 61 ESGVDRFTGSGMDPTLTISSVQAEADLWVYCONDYKPLTGGAGTKLEIKGGGGCG 120

QY 121 GGSQGGSEVOLLESGAELVRPGTSVKSACSYAFRNYLWQKPGQPPKLLIYASIR 180

Db 121 GGGGGGSEVOLLESGAELVRPGTSVKSACSYAFRNYLWQKPGQPPKLLIYASIR 180

QY 181 FPGSNIHTNEKFKSKATLTAKSSTANQQLSSITFEDSAVIFCARLNWDERMDYMQ 240

Db 181 FPGSNIHTNEKFKSKATLTAKSSTANQQLSSITFEDSAVIFCARLNWDERMDYMQ 240

QY 241 GTTVVVSSEGGGSDPIKLOSGAELARPGASVMSCKTSGTFTYTMVHKWQPGQGLEW 300

Db 241 GTTVVVSSEGGGSDPIKLOSGAELARPGASVMSCKTSGTFTYTMVHKWQPGQGLEW 300

QY 361 YMQGTTIVVSS 372

OS 361 YMQGTTIVVSS 372

DO 361 YMQGTTIVVSS 372

RESULT 9

AD283411

ID AD283411 standard; protein; 515 AA.

XX

AC AD283411;

XX

DT 14-JUL-2005 (first entry)

XX

DE Deimmunized construct 5-10xanti-CD3.

XX

DR neoplasm; inflammation; immune disorder; infection; allergy; graft versus host disease; Cytotoxic; Antiinflammatory; Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.

XX

OS Synthetic.

XX

PN WO2005040220-A1.

XX

PD 06-MAY-2005.

XX

PA (MICR-) MICROMET AG.

XX

PI Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Bauerle P;  
 Carr FU, Hamilton AA, Williams S;

XX DR WPI; 2005-333494/34.

XX DR N-FSDB; ADZ83440.

XX

PT New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g. proliferative disease.

PS Claim 20; SEQ ID NO 63; 639pp; English.

XX

CC The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, or allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft diseases. The cytotoxically active CD3 specific binding construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, or allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft diseases. The present sequence represents the amino acid sequence of deimmunized construct 5-10xanti-CD3.

XX

SQ Sequence 515 AA;

Query Match 92.5%; Score 1892; DB 9; Length 515;  
 Best Local Similarity 93.5%; Pred. No. 5.8e-110; Indels 0; Gaps 0;  
 Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 BLVMTQSPSLLTIVAGKVTMSCKSSQSLNSQNLNSQNLWYQKPGQPPKLLIYASIR 60

Db 20 ELVMTQSPSSLTVAGKVTMCKSSQDLSNQKNLTWQOKPGQPPKLUYWASTR 79  
 QY 61 ESGVDPDRFGSGSCTDFLTISVQAELAVYVQNDYSPLTFRGAGTKLEIKGGGG 120  
 Db 80 ESGVDPDRFGSGSCTDFLTISVQAELAVYVQNDYSPLTFRGAGTKLEIKGGGG 139  
 QY 121 GSGGGGSEVQOLBOSGAEVLVRGTSVKSCKASGAYAFTNYWLGWVKORPGHLEWQDI 180  
 Db 140 GSGGGGSEVQOLBOSGAEVLVRGTSVKSCKASGAYAFTNYWLGWVKORPGHLEWQDI 199  
 QY 181 PGSGNTHNEKFKCATLTADKSSTAYMQLSITFEDSAVFCARLNWDEPMYQ 240  
 Db 200 FPGSGNTHNEKFKCATLTADKSSTAYMQLSITFEDSAVFCARLNWDEPMYQ 259  
 QY 241 GTTVTVSSGGGSDTQLOSGAELARPAGASVMSKCKTSGVFTYTMHWKQRPGQLEW 300  
 Db 260 GTTVTVSSGGGSDTQLOSGAELARPAGASVMSKCKTSGVFTYTMHWKQRPGQLEW 319  
 QY 301 IGYINPSRGYTYNQKFKDQKATLTQDKSSSTAYMQLSITFEDSAVYVQNDYSPLTFRGAGTKLEIKGGGG 360  
 Db 320 IGYINPSRGYTYNQADFVKGRFTITQDKSSTAYMELLSRSEDATYVQARYYDDHCLD 379  
 QY 361 YWGQSTLTWSS 372  
 Db 380 YWGQSTLTWSS 391

RESULT 10

ID ADZ83641 standard; protein; 496 AA.  
 XX ADZ83641;  
 AC DT 14-JUL-2005 (first entry)  
 XX  
 DB CD3 specific binding construct SEQ ID NO 263.  
 XX  
 KW neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antinflammatory;  
 KW Immunosuppressive; Viricide; Antibacterial; Antiallergic; Antiparasitic.  
 XX  
 OS Synthetic.  
 XX  
 WO2005040220-A1.  
 XX  
 PD 06-MAY-2005.  
 XX  
 PF 15-OCT-2004; 2004WO-EP031646.  
 XX  
 PR 16-OCT-2003; 2003EP-00023581.  
 XX  
 PA (MICR-) MICROMET AG.

XX  
 PI Hofmeister R, Kohlheisen B, Ienkkeri-Schuetz U, Itin C, Bauerle P;  
 PI Carr FJ, Hamilton AA, Williams S;  
 XX  
 DR WPI; 2005-333494/34.  
 XX  
 N-PSDB; ADZ83640.

XX  
 PT New cytotoxicity active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g. proliferative disease.

XX  
 PS Claim 20, SEQ ID NO 263; 639pp; English.

XX  
 The invention relates to a cytotoxicity active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, an immunological

CC disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host disease, or host-versus-graft diseases. The cytotoxicity active CD3 specific binding construct is useful for treating, preventing, or ameliorating proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.

CC Sequence 496 AA:

Query Match 90.9%; Score 1859; DB 9; Length 496;  
 Best Local Similarity 71.6%; Pred. No. 6; e-108;  
 Matches 355; Conservative 11; Mismatches 6; Indels 124; Gaps 1;

Db 1 ELVMTQSPSSLTVAGKVTMCKSSQDLSNQKNLTWQOKPGQPPKLUYWASTR 60  
 QY 181 PGSGNTHNEKFKCATLTADKSSTAYMQLSITFEDSAVFCARLNWDEPMYQ 240  
 Db 121 GSGGGGSEVQOLBOSGAEVLVRGTSVKSCKASGAYAFTNYWLGWVKORPGHLEWQDI 180  
 QY 181 FPGSGNTHNEKFKCATLTADKSSTAYMQLSITFEDSAVFCARLNWDEPMYQ 259  
 Db 241 GTTVTVSSGGGSDTQLOSGAELARPAGASVMSKCKTSGVFTYTMHWKQRPGQLEW 300  
 QY 241 GTTVTVSSGGGSDTQLOSGAELARPAGASVMSKCKTSGVFTYTMHWKQRPGQLEW 319  
 Db 241 GTTVTVSSGGGSDTQLOSGAELARPAGASVMSKCKTSGVFTYTMHWKQRPGQLEW 320  
 QY 301 YDTSKVAVSGVPARFSGSGGSDTSLTINLEAEDAATYVQQMSNSNPLTFGGGTKEVKG 360  
 Db 320 IGYINPSRGYTYNQKFKDQKATLTQDKSSSTAYMQLSITFEDSAVYVQNDYSPLTFRGAGTKLEIKGGGG 360  
 QY 320 IGYINPSRGYTYNQADFVKGRFTITQDKSSTAYMELLSRSEDATYVQARYYDDH 379  
 Db 361 EGSTGSGGGGSDTQLOSGAELARPAGASVMSKCKTSGVFTYTMHWKQRPGQ 420  
 QY 361 EGSTGSGGGGSDTQLOSGAELARPAGASVMSKCKTSGVFTYTMHWKQRPGQ 420  
 Db 421 GLEWIGYINPSRGYTYNQKFKDQKATLTQDKSSSTAYMQLSITFEDSAVYVQNDYSPLTFRGAGTKLEIKGGGG 480  
 QY 421 GLEWIGYINPSRGYTYNQKFKDQKATLTQDKSSSTAYMQLSITFEDSAVYVQNDYSPLTFRGAGTKLEIKGGGG 480  
 Db 481 YCLDWGQSTLTWSS 496  
 QY 481 YCLDWGQSTLTWSS 496

RESULT 11

ID ADZ83649 standard; protein; 496 AA.  
 XX  
 AC ADZ83649;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DB CD3 specific binding construct SEQ ID NO 271.  
 XX  
 KW neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antinflammatory;  
 KW Immunosuppressive; Viricide; Antibacterial; Antiallergic; Antiparasitic.  
 XX  
 OS Synthetic.

XX  
 WO2005040220-A1.  
 XX  
 PD 06-MAY-2005.



Db 61 ESGVDRFTGSGSDTDFITISSVQAEIDLAVYCONDYSIPTLGAGTKEIKGGSGC 120  
 QY 121 GSGGGGSEVOLLQSGASLVRPGTSVKISKASQYAFNTWLGWVQKQPGHGLEWGI 180  
 Db 121 GSGGGGSEVOLLQSGASLVRPGTSVKISKASQYAFNTWLGWVQKQPGHGLEWGI 180  
 CC disorder, an autoimmune disease, an infectious disease, viral disease, or  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease, or  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of deimmunized construct 4-ixanti-CD3.  
 XX

QY 241 GTTVTVSSGGGSDIVLQSPATLSPGERATLTCRASSSVSTMWYQQKPGKAPKRW 300  
 Db 241 GTTVIVSSGGGSDIVLQSPATLSPGERATLTCRASSSVSTMWYQQKPGKAPKRW 300  
 CC  
 QY 256 - 255  
 Db 301 YDTSKVAVGVPARFSGSGSDTDSLTSNLEAEDATYQQQSNPLFGGGKVEKG 360  
 QY 256 - KLOQSGAELARPAGSVMCKTSQGTYPTRYTMHWKQRPQG 295  
 Db 361 EGTSSTGSGGGGGADDYQVQLVSGAEVKPGASVVKISKASQYFTPTRYTMHWQARQG 420  
 QY 297 GLEWGYINNSRGYVNYNQKEKQDALKTITKSSSTAYMOLSLTSEDAVYCARYYDDH 356  
 Db 421 GLEWGYINNSRGYVNYNQKEKQDALKTITKSSSTAYMOLSLTSEDAVYCARYYDDH 480  
 QY 357 YCLDYGQGTTLTVSS 372  
 Db 481 YCLDYGQGTTLTVSS 496

RESULT 13

Db AD283436 standard; protein; 515 AA.  
 ID AD283436:  
 XX AC  
 XX DT 14-JUL-2005 (first entry)  
 XX DE Deimmunized construct 4-ixanti-CD3.  
 XX KW neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antinflammatory;  
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.  
 XX OS Synthetic.  
 XX PN WO2005040220-A1.  
 XX PD 06-MAY-2005.  
 XX PR 15-OCT-2004; 2004WO-BP011646.  
 XX PR 16-OCT-2003; 2003EP-00023581.  
 XX DA (MICR-) MICROMET AG.  
 PI Hofmäster R, Kohlisen B, Jenkner-Schuetz U, Itin C, Baerle P;  
 PI Carr RJ, Hamilton AA, Williams S;  
 DR WPI, 2005-33349/34.  
 XX N-PSDB; AD283435.

New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g. proliferative disease.

PS Claim 20; SEQ ID NO 58; 639pp; English.

CC The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and

Query Match 89.4%; Score 1829; DB 9; Length 515;  
 Local Similarity 90.6%; Pred. No. 4.96-106; Matches 337; Conservative 15; Mismatches 20; Indels 0; Gaps 0;  
 Matches 337; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Db 1 ELWMTQS PSLVITVAGEKTYMCKTSQSSUQNLNSGQKNTLTWQOKPGQPKLILWASTR 60  
 QY 20 ELWMTQS PSLVITVAGEKTYMCKTSQSSUQNLNSGQKNTLTWQOKPGQPKLILWASTR 79

Db 61 ESGVDRFTGSGSDTDFITISSVQAEIDLAVYCONDYSIPTLGAGTKEIKGGSGC 120  
 QY 80 ESGVDRFTGSGSDTDFITISSVQAEIDLAVYCONDYSIPTLGAGTKEIKGGGSG 139

QY 121 GSGGGGSEVOLLQSGASLVRPGTSVKISKASQYAFNTWLGWVQKQPGHGLEWGI 180  
 Db 140 GGSGGGSEVOLLQSGASLVRPGTSVKISKASQYAFNTWLGWVQKQPGHGLEWGI 199  
 QY 181 FPGSGNITHMEKFKKATLTADKSSSTAYMOLSLTSEDAVYCARLWRDEPMYQG 240  
 Db 200 FPGSGNITHMEKFKKATLTADKSSSTAYMOLSLTSEDAVYCARLWRDEPMYQG 259

Db 241 GTTVTVSSGGGSDIVLQSGAELARPAGSVMCKTSQGTYPTRYTMHWKQRPQG 300  
 QY 260 GTTVIVSSGGGSDIVLQSGAEVKPGASVVKISKASQYFTPTRYTMHWQARQGLEN 319

Db 301 IGYINNSRGYVNYNQKEKQDALKTITKSSSTAYMOLSLTSEDAVYCARYYDDH 360  
 QY 320 IGYINNSRGYVNYNQKEKQDALKTITKSSSTAYMOLSLTSEDAVYCARYYDDH 379

Db 361 YWGQGTTLTVSS 372  
 QY 380 YWGQGTTLTVSS 391

RESULT 14

Db AD283619 standard; protein; 496 AA.  
 ID AD283619:  
 XX AC  
 XX DT 14-JUL-2005 (first entry)  
 XX DE CD3 specific binding construct SEQ ID NO 241.  
 XX KW neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antinflammatory;  
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.  
 XX OS Synthetic.  
 XX PN WO2005040220-A1.  
 XX PD 06-MAY-2005.  
 XX PR 15-OCT-2004; 2004WO-BP011646.  
 XX PR 16-OCT-2003; 2003EP-00023581.

DB	481 YCLDYWGCGTTVVS 496
XX	
PA	
XX	(MICR-) MICROMET AG.
PI	
PI	Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Bauerle P;
PI	Carr FU, Hamilton AA, Williams S;
XX	
DR	WPI; 2005-333494/34.
DR	N-PSDB; AD283618.
XX	
PT	New cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g. proliferative disease.
PT	domain specifically binding to human CD3 and an Ig-derived second binding domain, useful for treating, preventing, or ameliorating, e.g. proliferative disease.
XX	
PS	Claim 20; SEQ ID NO 241; 639pp; English.
XX	
CC	The invention relates to a cytotoxically active CD3 specific binding construct comprises a first domain specifically binding to human CD3 and an Ig-derived second binding domain. The CD3 specific binding construct above or the construct produced by the process, nucleic acid molecule, vector, or host is useful for the preparation of a pharmaceutical composition for the prevention, treatment, or amelioration of a proliferative disease, a tumor, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, or host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.
CC	
CC	host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.
CC	
CC	host-versus-graft diseases. The present sequence represents the amino acid sequence of a CD3 specific binding construct.
XX	
SQ	Sequence 496 AA;
Query Match	89.0%; Score 1821; DB 9; Length 496;
Best Local Similarity	70.4%; Pred. No. 1.5e-105;
Matches	349; Conservative 11; Mismatches 12; Indels 124; Gaps 1;
QY	
1	ELWVQSPSITIVTAGEKVYTMCKSSQSILNSNQKVNLTWQOKPGCGPPKKLIIWASTR 60
Db	
1	ELWVQSPSITIVTAGEKVYTMCKSSQSILNSNQKVNLTWQOKPGCGPPKKLIIWASTR 60
QY	
61	ESGYVDRFTGSGSGTDFITISVQAEILAVYCONDYSYPLTFAGKLEIKGGGGGG 120
Db	
61	ESGYVDRFTGSGSGTDFITISVQAEILAVYCONDYSYPLTFAGKLEIKGGGGGG 120
QY	
121	GGSGGGSEVQOLBQGABEVRPGTISKVLSCKASGYAFTNWLGWVKORPGHGLEWIGDI 180
Db	
121	GGSGGGSEVQOLBQGABEVRPGTISKVLSCKASGYAFTNWLGWVKORPGHGLEWIGDI 180
QY	
181	FGPGSNIHMKFKKATLADKSSTATWQLSLTFEASAAYVCARLWNMDPMDYQ 240
Db	
181	FGPGSNIHMKFKKATLADKSSTATWQLSLTFEASAAYVCARLWNMDPMDYQ 240
QY	
241	GTTTVVSSGGGSDI----- 255
Db	
241	GTTTVVSSGGGSDIOMTQSPSSLASAVGDRVTITCRASQSVSTNNWYQOKPGKPKW 300
QY	
256	----- 255
QY	
301	YDTSKVAVSGVPPARFGSGSGTDSLTINSLRAEDATYQQWSNPLTPGGTKEVKG 360
Db	
256	----- 256
QY	
361	EGTGSTGSGGGGGGADDVQVQSAEVKPGAGTFSKCKASGTTFRTMHWQAPQ 420
Db	
297	GLEMIGYINPSRGYTYNQKEDKATLTDKSSSTAYMOLSLTSBDSAVYCARVYDDH 356
Db	
421	GLEWIGYINPSRGYTYNQDSVKGRFTITDQSTSTAYMULSLRSEDATYCARVYDDH 480
QY	
357	YCLDYWGQGTLTWVS 372
QY	
Query Match	89.0%; Score 1821; DB 9; Length 496;
Best Local Similarity	70.4%; Pred. No. 1.5e-105;
Matches	349; Conservative 11; Mismatches 12; Indels 124; Gaps 1;
QY	
1	ELWVQSPSITIVTAGEKVYTMCKSSQSILNSNQKVNLTWQOKPGCGPPKKLIIWASTR 60
Db	
61	ESGYVDRFTGSGSGTDFITISVQAEILAVYCONDYSYPLTFAGKLEIKGGGGGG 120
QY	
61	ESGYVDRFTGSGSGTDFITISVQAEILAVYCONDYSYPLTFAGKLEIKGGGGGG 120

Qy 121 GGS CGG SEV QLLE SGA ELV R PGT SKV LSC KAS GY AFT NY WLG V KOR PG HGL EWI GDI 180  
 Db 121 GGS CGG SEV QLLE SGA ELV R PGT SKV LSC KAS GY AFT NY WLG V KOR PG HGL EWI GDI 180  
 Qy 181 PPG SNI HTE KFK KAT LDA KSS STAY MOI LS LT PFD SAV Y CARY LND EPM D YGQ 240  
 Db 181 PPG SNI HTE KFK KAT LDA KSS STAY MOI LS LT PFD SAV Y CARY LND EPM D YGQ 240  
 Qy 241 GTT VTV SSG GGS D1----- 255  
 Db 241 GTT VTV SSG GGS D1----- 255  
 Qy 256 ----- 255  
 Db 301 YDT SKV ASGV PAR FSG SGT DYS LT INS LFA D A T Y CQW S N P L T F G G T K V E I K G 360  
 Qy 256 ----- 296  
 Db 361 EGT STG SGG SGS GGA D D V QSG A E V K K P G A S V R K V S C K A S G Y P T R Y H W V K O R P G O 420  
 Qy 297 GLE WIG Y IN P R G Y T N N Q K F R D K A T L T D K S S STAY MOI LS LT PFD SAV Y CARY DDH 356  
 Db 421 GLE WIG Y IN P R G Y T N N Q K F R D K A T L T D K S S STAY MOI LS LT PFD SAV Y CARY DDH 480  
 Qy 357 YCL DY W QG T V T V S S 372  
 Db 481 YCL DY W QG T V T V S S 496

Search completed: March 6, 2006, 14:46:23  
 Job time : 91 sec<sub>B</sub>

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